

WE CLAIM THE FOLLOWING:

1. An isolated terpene synthase having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, said synthase comprising nine  $\alpha$ -carbons having interatomic distances in Angstroms between said  $\alpha$ -carbons that are  $\pm 2.3$  Angstroms of the following interatomic distances:

| $\alpha$ -Carbon | 1    | 2    | 3    | 4    | 5    | 6    | 7    | 8    | 9    |
|------------------|------|------|------|------|------|------|------|------|------|
| 1                | 0.0  | 8.4  | 13.7 | 12.7 | 11.9 | 10.2 | 13.1 | 9.4  | 12.8 |
| 2                | 8.4  | 0.0  | 11.3 | 8.7  | 10.2 | 7.2  | 14.8 | 15.1 | 17.4 |
| 3                | 13.7 | 11.3 | 0.0  | 3.8  | 5.4  | 9.3  | 6.6  | 13.9 | 13.7 |
| 4                | 12.7 | 8.7  | 3.8  | 0.0  | 3.8  | 6.0  | 9.2  | 15.4 | 16.1 |
| 5                | 11.9 | 10.2 | 5.4  | 3.8  | 0.0  | 5.0  | 7.8  | 14.6 | 15.5 |
| 6                | 10.2 | 7.2  | 9.3  | 6.0  | 5.0  | 0.0  | 12.0 | 16.1 | 18.0 |
| 7                | 13.1 | 14.8 | 6.6  | 9.2  | 7.8  | 12.0 | 0.0  | 10.2 | 9.5  |
| 8                | 9.4  | 15.1 | 13.9 | 15.4 | 14.6 | 16.1 | 10.2 | 0.0  | 3.8  |
| 9                | 12.8 | 17.4 | 13.7 | 16.1 | 15.5 | 18.0 | 9.5  | 3.8  | 0.0  |

the center point of each said  $\alpha$ -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center points of each said sphere having the following structural coordinates:

| $\alpha$ -Carbon Number | X Position | Y Position | Z Position |
|-------------------------|------------|------------|------------|
| 1                       | 120.203    | 38.695     | 43.506     |
| 2                       | 114.058    | 43.884     | 41.015     |
| 3                       | 106.807    | 36.336     | 45.151     |
| 4                       | 107.629    | 38.010     | 41.804     |
| 5                       | 109.375    | 34.842     | 40.617     |
| 6                       | 111.944    | 37.854     | 37.602     |
| 7                       | 110.233    | 31.098     | 47.361     |
| 8                       | 118.846    | 34.443     | 51.796     |
| 9                       | 116.461    | 32.848     | 54.290     |

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, each said  $\alpha$ -carbon having an associated R-group, said synthase having an ordered arrangement of said R-groups other than the following ordered arrangements of R-groups:

Table 9

| Ordered Arrangements of $\alpha$ -Carbons 1-9 |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|
|   | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
| A   | W | I | T | T | Y | L | C | T | Y |
| B   | W | I | S | T | Y | L | C | T | Y |
| C   | W | I | C | G | Y | L | C | L | Y |
| D   | W | I | S | G | Y | L | C | L | Y |
| E   | W | L | A | G | Y | I | A | L | Y |
| F   | W | L | T | V | H | L | G | V | Y |
| G   | W | L | A | G | Y | I | A | L | Y |
| H   | W | I | V | G | N | L | F | L | Y |
| I   | W | I | T | A | G | L | S | C | Y |
| J   | W | V | S | C | I | M | G | S | Y |
| K   | F | F | I | T | A | T | G | T | Y |
| L   | W | N | I | S | G | M | L | M | Y |
| M   | W | V | S | S | Y | L | G | L | Y |
| N   | F | F | T | L | A | L | G | S | Y |
| O   | W | N | S | G | P | L | L | M | Y |
| P   | W | N | G | G | I | L | L | I | Y |
| Q   | Y | L | V | T | M | T | G | T | Y |
| R   | W | I | I | S | A | I | L | I | Y |
| S   | W | F | S | S | V | I | L | I | Y |
| T   | W | I | V | A | S | I | L | I | Y |
| U   | W | N | I | S | S | I | F | M | Y |
| V   | L | A | I | G | Q | L | S | I | F |
| W   | S | S | I | A | L | V | G | F | Y |
| X   | L | C | C | G | H | S | L | G | Y |
| Y   | S | F | S | S | V | I | L | V | Y |
| Z   | W | A | S | G | M | L | G | I | Y |

Table 9

|    |   |   |   |   |   |   |   |   |   |
|----|---|---|---|---|---|---|---|---|---|
| AA | A | N | L | T | S | T | C | L | Y |
| BB | L | C | S | A | Y | V | L | L | Y |
| CC | W | A | T | G | M | L | S | M | Y |
| DD | M | C | S | S | G | I | L | V | Y |
| EE | S | G | V | G | L | C | W | F | Y |
| FF | S | G | A | L | G | V | G | F | Y |
| GG | S | G | F | A | L | I | G | F | Y |
| HH | A | G | F | A | L | I | G | F | Y |
| II | W | V | T | G | L | V | I | S | Y |
| JJ | W | A | S | G | M | L | G | I | Y |
| KK | W | I | S | T | Y | L | C | T | Y |
| LL | W | I | T | T | Y | L | C | T | Y |
| MM | W | N | I | S | G | M | L | M | Y |
| NN | A | A | I | G | Q | L | S | I | F |
| OO | A | I | V | A | S | I | L | I | Y |

2. The synthase of claim 1, wherein said synthase has 25% or greater sequence identity to residues 265 to 535 of SEQ ID 2.
- 5 3. The synthase of claim 2, wherein said synthase has 35% or greater sequence identity to residues 265 to 535 of SEQ ID 2.
4. The synthase of claim 1, wherein said synthase catalyses the formation of a terpenoid product from a monoterpene substrate.
- 10 5. The synthase of claim 1, wherein said synthase catalyses the formation of a terpenoid product from a sesquiterpene substrate.
6. The synthase of claim 1, wherein said synthase catalyses the formation of a terpenoid product from a diterpene substrate.
- 15 7. The synthase of claims 4, 5, or 6, wherein said product is a cyclic terpenoid hydrocarbon.
- 20 8. The synthase of claim 4, 5, or 6, wherein said product is an acyclic terpenoid hydrocarbon.
9. The synthase of claim 4, 5, or 6 wherein said product is a cyclic hydroxylated terpenoid hydrocarbon.
- 25 10. The synthase of claim 4, 5, or 6 wherein said product is an acyclic hydroxylated terpenoid hydrocarbon.
11. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 1 is selected from the group consisting of Cys, Ser, and Thr.
- 30 12. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 1 is selected from the group consisting of Phe, Tyr and Trp.

13. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 1 is selected from the group consisting of Pro, Gly, and Ala.

14. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 1 is selected from the group consisting of Glu and Asp.

15. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 1 is selected from the group consisting of Met, Ile, Val and Leu.

16. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 1 is selected from the group consisting of Arg and Lys.

17. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 1 is selected from the group consisting of Gln, Asn and His.

18. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 2 is selected from the group consisting of Cys, Ser and Thr.

19. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 2 is selected from the group consisting of Phe, Tyr and Trp.

20. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 2 is selected from the group consisting of Pro, Gly, and Ala.

21. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 2 is selected from the group consisting of Glu and Asp.

22. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 2 is selected from the group consisting of Met, Ile, Val and Leu.

23. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 2 is selected from the group consisting of Arg and Lys.

24. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 2 is selected from the group consisting of Gln, Asn and His.

25. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 3 is selected from the group consisting of Cys, Ser and Thr.
- 5 26. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 3 is selected from the group consisting of Phe, Tyr and Trp.
27. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 3 is selected from the group consisting of Pro, Gly, and Ala.
- 10 28. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 3 is selected from the group consisting of Glu and Asp.
29. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 3 is selected from the group consisting of Met, Ile, Val and Leu.
- 15 30. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 3 is selected from the group consisting of Arg and Lys.
31. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 3 is selected from the group consisting of Gln, Asn and His.
- 20 32. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 4 is selected from the group consisting of Cys, Ser and Thr.
- 25 33. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 4 is selected from the group consisting of Phe, Tyr and Trp.
34. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 4 is selected from the group consisting of Pro, Gly, and Ala.
- 30 35. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 4 is selected from the group consisting of Glu and Asp.

36. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 4 is selected from the group consisting of Met, Ile, Val and Leu.
37. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 4 is selected from the group consisting of Arg and Lys.
38. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 4 is selected from the group consisting of Gln, Asn and His.
39. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 5 is selected from the group consisting of Cys, Ser and Thr.
40. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 5 is selected from the group consisting of Phe, Tyr and Trp.
41. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 5 is selected from the group consisting of Pro, Gly, and Ala.
42. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 5 is selected from the group consisting of Glu and Asp.
43. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 5 is selected from the group consisting of Met, Ile, Val and Leu.
44. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 5 is selected from the group consisting of Arg and Lys.
45. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 5 is selected from the group consisting of Gln, Asn and His.
46. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 6 is selected from the group consisting of Cys, Ser and Thr.
47. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 6 is selected from the group consisting of Phe, Tyr and Trp.

48. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 6 is selected from the group consisting of Pro, Gly, and Ala.

5 49. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 6 is selected from the group consisting of Glu and Asp.

50. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 6 is selected from the group consisting of Met, Ile, Val and Leu.

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51. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 6 is selected from the group consisting of Arg and Lys.

52. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 6 is selected from the group consisting of Gln, Asn and His.

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53. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 7 is selected from the group consisting of Cys, Ser and Thr.

20 54. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 7 is selected from the group consisting of Phe, Tyr and Trp.

55. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 7 is selected from the group consisting of Pro, Gly, and Ala.

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56. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 7 is selected from the group consisting of Glu and Asp.

57. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 7 is selected from the group consisting of Met, Ile, Val and Leu.

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58. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 7 is selected from the group consisting of Arg and Lys.



59. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 7 is selected from the group consisting of Gln, Asn and His.
60. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 3 is selected from the group consisting of Cys, Ser and Thr.
61. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 8 is selected from the group consisting of Phe, Tyr and Trp.
62. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 8 is selected from the group consisting of Pro, Gly, and Ala.
63. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 8 is selected from the group consisting of Glu and Asp.
64. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 8 is selected from the group consisting of Met, Ile, Val and Leu.
65. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 8 is selected from the group consisting of Arg and Lys.
66. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 8 is selected from the group consisting of Gln, Asn and His.
67. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 9 is selected from the group consisting of Cys, Ser and Thr.
68. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 9 is selected from the group consisting of Phe, Tyr and Trp.
69. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 9 is selected from the group consisting of Pro, Gly, and Ala.
70. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 9 is selected from the group consisting of Glu and Asp.

71. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 9 is selected from the group consisting of Met, Ile, Val and Leu.

5 72. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 9 is selected from the group consisting of Arg and Lys.

73. The synthase of claim 1, wherein said R-group associated with said  $\alpha$ -carbon 9 is selected from the group consisting of Gln, Asn and His.

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74. The synthase of claim 1, wherein said ordered arrangement of R-groups in said synthase associated with said  $\alpha$ -carbons 1 to 9 is Trp, Ile, Thr, Thr, Tyr, Leu, Cys, Thr and Phe, respectively.

15 75. The synthase of claim 1, wherein said ordered arrangement of R-groups in said synthase associated with said  $\alpha$ -carbons 1 to 9 is Ser, Ile, Thr, Thr, Tyr, Leu, Cys, Thr and Tyr, respectively.

20 76. The synthase of claim 1, wherein said ordered arrangement of R-groups in said synthase associated with said  $\alpha$ -carbons 1 to 9 is Trp, Ile, Thr, Thr, Tyr, Leu, Trp, Thr and Tyr, respectively.

25 77. The synthase of claim 1, wherein said ordered arrangement of R-groups in said synthase associated with said  $\alpha$ -carbons 1 to 9 is Ser, Ile, Thr, Thr, Tyr, Leu, Trp, Thr and Tyr, respectively.

30 78. The synthase of claim 1, wherein said ordered arrangement of R-groups in said synthase associated with said  $\alpha$ -carbons 1 to 9 is Glu, Ile, Thr, Thr, Tyr, Leu, Cys, Thr and Tyr, respectively.

35 79. A terpene synthase made by aligning a primary amino acid sequence of a terpene synthase polypeptide to the amino acid sequence of residues 265 to 535 of SEQ ID NO: 2, mutating a nucleic acid encoding said polypeptide at one or more codons of nine amino acid residues in a region of said polypeptide having 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, said nine residues

in said polypeptide aligning with residues 273, 294, 402, 403, 404, 407, 440, 519 and 520 of SEQ ID NO: 2; and expressing said mutated nucleic acid so that a mutated terpene synthase is made.

- 5 80. An isolated terpene synthase having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, said synthase comprising sixteen  $\alpha$ -carbons, said  $\alpha$ -carbons having interatomic distances in Angstroms between said  $\alpha$ -carbons that are  $\pm 2.3$  Angstroms of the following interatomic distances:

1.08290" 02886860

| $\alpha$ -Carbon | 1    | 2    | 3    | 4    | 5    | 6    | 7    | 8    | 9    | 10   | 11   | 12   | 13   | 14   | 15   | 16   |
|------------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1                | 0.0  | 5.0  | 6.0  | 10.5 | 9.0  | 14.3 | 13.0 | 13.5 | 11.2 | 15.6 | 12.5 | 11.8 | 15.0 | 13.7 | 8.3  | 11.0 |
| 2                | 5.0  | 0.0  | 8.4  | 13.3 | 12.4 | 13.7 | 12.7 | 11.9 | 10.2 | 13.1 | 9.2  | 9.4  | 12.8 | 13.6 | 9.3  | 12.9 |
| 3                | 6.0  | 8.4  | 0.0  | 5.3  | 6.0  | 11.3 | 8.7  | 10.2 | 7.2  | 14.8 | 13.9 | 15.1 | 17.4 | 15.7 | 11.3 | 13.3 |
| 4                | 10.5 | 13.3 | 5.3  | 0.0  | 3.8  | 10.7 | 8.3  | 11.4 | 9.6  | 16.1 | 16.8 | 18.1 | 19.6 | 16.8 | 13.3 | 13.9 |
| 5                | 9.0  | 12.4 | 6.0  | 3.8  | 0.0  | 10.8 | 9.6  | 12.5 | 11.6 | 15.5 | 15.4 | 15.9 | 17.3 | 13.8 | 10.1 | 10.3 |
| 6                | 14.3 | 13.7 | 11.3 | 10.7 | 10.8 | 0.0  | 3.8  | 5.4  | 9.3  | 6.6  | 10.5 | 13.9 | 13.7 | 12.9 | 12.8 | 14.1 |
| 7                | 13.0 | 12.7 | 8.7  | 8.3  | 9.6  | 3.8  | 0.0  | 3.8  | 6.0  | 9.2  | 12.1 | 15.4 | 16.1 | 15.3 | 13.8 | 15.4 |
| 8                | 13.5 | 11.9 | 10.2 | 11.4 | 12.5 | 5.4  | 3.8  | 0.0  | 5.0  | 7.8  | 10.5 | 14.6 | 15.5 | 16.0 | 14.7 | 17.0 |
| 9                | 11.2 | 10.2 | 7.2  | 9.6  | 11.6 | 9.3  | 6.0  | 5.0  | 0.0  | 12.0 | 12.8 | 16.1 | 18.0 | 18.2 | 15.3 | 17.8 |
| 10               | 15.6 | 13.1 | 14.8 | 16.1 | 15.5 | 6.6  | 9.2  | 7.8  | 12.0 | 0.0  | 5.9  | 10.2 | 9.5  | 11.4 | 12.8 | 14.9 |
| 11               | 12.5 | 9.2  | 13.9 | 16.8 | 15.4 | 10.5 | 12.1 | 10.5 | 12.8 | 5.9  | 0.0  | 5.0  | 6.0  | 9.5  | 9.7  | 12.8 |
| 12               | 11.8 | 9.4  | 15.1 | 18.1 | 15.9 | 13.9 | 15.4 | 14.6 | 16.1 | 12.2 | 5.0  | 0.0  | 3.8  | 7.1  | 7.2  | 10.2 |
| 13               | 15.0 | 12.8 | 17.4 | 19.6 | 17.3 | 13.7 | 16.1 | 15.5 | 18.0 | 9.5  | 6.0  | 3.8  | 0.0  | 5.8  | 8.8  | 10.8 |
| 14               | 13.7 | 13.6 | 15.7 | 16.8 | 13.8 | 12.9 | 15.3 | 16.0 | 18.2 | 11.4 | 9.5  | 7.1  | 5.8  | 0.0  | 5.7  | 5.7  |
| 15               | 8.3  | 9.3  | 11.3 | 13.3 | 10.1 | 12.8 | 13.8 | 14.7 | 15.3 | 12.8 | 9.7  | 7.2  | 8.8  | 5.7  | 0.0  | 3.8  |
| 16               | 11.0 | 12.9 | 13.3 | 13.9 | 10.3 | 14.1 | 15.4 | 17.0 | 17.8 | 14.9 | 12.8 | 10.2 | 10.8 | 5.7  | 3.8  | 0.0  |

the center point of each said  $\alpha$ -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center points of each said sphere having the following structural coordinates:

| $\alpha$ -Carbon Number | X Position | Y Position | Z Position |
|-------------------------|------------|------------|------------|
| 1                       | 119.144    | 43.487     | 44.133     |
| 2                       | 120.203    | 38.695     | 43.506     |
| 3                       | 114.058    | 43.884     | 41.015     |
| 4                       | 109.327    | 46.145     | 41.743     |
| 5                       | 110.682    | 46.410     | 45.284     |
| 6                       | 106.807    | 36.336     | 45.151     |
| 7                       | 107.629    | 38.010     | 41.804     |
| 8                       | 109.375    | 34.842     | 40.617     |
| 9                       | 111.944    | 37.854     | 37.602     |
| 10                      | 110.233    | 31.098     | 47.361     |
| 11                      | 115.915    | 32.218     | 48.369     |
| 12                      | 118.846    | 34.443     | 51.796     |
| 13                      | 116.461    | 32.848     | 54.290     |
| 14                      | 114.100    | 38.006     | 55.620     |
| 15                      | 116.617    | 41.285     | 51.702     |
| 16                      | 114.855    | 43.486     | 54.238     |

, each said  $\alpha$ -carbon having an associated R-group, said synthase having an ordered arrangement of said R-groups other than the following ordered arrangements of R-groups:

Table 8

| Ordered Arrangement of R-Groups at $\alpha$ -carbons 1-16 |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |
|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|
|   | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
| A   | C | W | I | I | S | T | T | Y | L | C  | V  | T  | Y  | D  | Y  | T  |
| B   | C | W | I | I | S | S | T | Y | L | C  | I  | T  | Y  | D  | Y  | T  |
| C   | G | W | I | A | S | C | G | Y | L | C  | M  | L  | Y  | D  | Y  | T  |
| D   | G | W | I | A | S | S | G | Y | L | C  | M  | L  | Y  | D  | Y  | T  |
| E   | C | W | L | T | S | A | G | Y | I | A  | A  | L  | Y  | D  | Y  | T  |
| F   | G | W | L | L | S | T | V | H | L | G  | A  | V  | Y  | D  | Y  | T  |
| G   | C | W | L | T | S | A | G | Y | I | A  | A  | L  | Y  | D  | Y  | T  |
| H   | L | W | I | T | T | V | G | N | L | F  | V  | L  | Y  | D  | Y  | T  |
| I   | P | W | I | V | D | T | A | G | L | S  | A  | C  | Y  | D  | Y  | T  |
| J   | A | W | V | C | G | S | C | I | M | G  | C  | S  | Y  | D  | Y  | T  |
| K   | N | F | F | L | G | I | T | A | T | G  | I  | T  | Y  | D  | Y  | T  |
| L   | C | W | N | I | T | I | S | G | M | L  | A  | M  | Y  | D  | Y  | T  |
| M   | S | W | V | L | T | S | S | Y | L | G  | V  | L  | Y  | D  | Y  | T  |
| N   | N | F | F | L | V | T | L | A | L | G  | L  | S  | Y  | D  | Y  | T  |
| O   | C | W | N | I | T | S | G | P | L | L  | A  | M  | Y  | D  | Y  | T  |
| P   | C | W | N | V | T | G | G | I | L | L  | A  | I  | Y  | D  | Y  | T  |
| Q   | C | Y | L | L | T | V | T | M | T | G  | I  | T  | Y  | D  | Y  | T  |
| R   | C | W | I | I | T | I | S | A | I | L  | A  | I  | Y  | D  | Y  | T  |
| S   | S | W | F | I | V | S | S | V | I | L  | V  | I  | Y  | D  | Y  | T  |
| T   | S | W | I | A | T | V | A | S | I | L  | A  | I  | Y  | D  | Y  | T  |
| U   | N | W | N | L | T | I | S | S | I | F  | S  | M  | Y  | D  | Y  | T  |
| V   | F | L | A | Q | T | I | G | Q | L | S  | T  | I  | F  | D  | Y  | T  |
| W   | I | S | S | T | V | I | A | L | V | G  | M  | F  | Y  | D  | Y  | T  |
| X   | Y | L | C | I | T | C | G | H | S | L  | F  | G  | Y  | D  | Y  | T  |
| Y   | G | S | F | I | T | S | S | V | I | L  | A  | V  | Y  | D  | Y  | T  |
| Z   | Y | W | A | C | T | S | G | M | L | G  | L  | I  | Y  | D  | Y  | T  |

Table 8

|    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AA | A | A | N | L | T | L | T | S | T | C | L | L | L | Y | D | Y | N |
| BB | F | L | C | V | T | S | T | Y | V | L | L | L | L | Y | D | F | S |
| CC | F | W | A | M | T | T | G | M | L | S | I | I | M | Y | D | F | S |
| DD | Y | M | C | V | T | S | S | G | I | L | F | V | V | Y | D | Y | T |
| EE | V | S | G | Q | V | V | G | L | C | W | V | V | F | Y | D | Y | G |
| FF | C | S | G | T | T | A | L | G | V | G | L | L | F | Y | D | F | T |
| GG | C | S | G | T | T | F | A | L | I | G | L | L | F | Y | D | F | T |
| HH | C | A | G | T | T | F | A | L | I | G | V | V | F | Y | D | Y | T |
| II | I | W | V | I | S | T | G | L | V | I | T | T | S | Y | D | Y | T |
| JJ | Y | W | A | C | T | S | G | M | L | G | L | L | I | Y | D | L | Y |
| KK | C | W | I | I | S | S | T | Y | L | C | V | I | T | Y | D | Y | T |
| LL | C | W | I | I | S | T | T | Y | L | C | I | I | T | Y | D | Y | T |
| MM | C | W | N | I | T | I | S | G | M | L | A | A | M | Y | D | H | G |
| NN | F | A | A | Q | T | I | G | Q | L | S | T | I | I | F | D | F | G |
| OO | F | A | I | A | T | V | A | S | I | L | A | A | I | Y | D | F | G |

81. The synthase of claim 80, wherein said synthase has 25% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2.
82. The synthase of claim 81, wherein said synthase has 35% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2.
83. The synthase of claim 81, wherein said synthase catalyses the formation of a terpenoid product from a monoterpene substrate.
84. The synthase of claim 81, wherein said synthase catalyses the formation of a terpenoid product from a sesquiterpene substrate.
85. The synthase of claim 81, wherein said synthase catalyses the formation of a terpenoid product from a diterpene substrate.
86. The synthase of claims 83, 84, or 85, wherein said product is a cyclic terpenoid hydrocarbon.
87. The synthase of claim 81, wherein said ordered arrangement of R-groups in said synthase associated with said  $\alpha$ -carbons 1 to 16 is Cys, Trp, Ile, Ile, Ser, Thr, Thr, Tyr, Leu, Cys, Val, Thr, Tyr, Asp, Phe and Thr, respectively.
88. An isolated terpene synthase having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, said synthase comprising nineteen  $\alpha$ -carbons having interatomic distances in Angstroms between said  $\alpha$ -carbons that are  $\pm 2.3$  Angstroms of the following interatomic distances:



Table 2

| $\alpha$ -carbon | 1    | 2    | 3    | 4    | 5    | 6    | 7    | 8    | 9    | 10   | 11   | 12   | 13   | 14   | 15   | 16   | 17   | 18   | 19   |
|------------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1                | 0.0  | 5.0  | 6.0  | 10.5 | 9.0  | 19.8 | 16.6 | 14.3 | 13.0 | 13.5 | 11.2 | 15.6 | 16.7 | 12.5 | 11.8 | 15.0 | 13.7 | 8.3  | 11.0 |
| 2                | 5.0  | 0.0  | 8.4  | 13.3 | 12.4 | 21.3 | 16.8 | 13.7 | 12.7 | 11.9 | 10.2 | 13.1 | 15.4 | 9.2  | 9.4  | 12.8 | 13.6 | 9.3  | 12.9 |
| 3                | 6.0  | 8.4  | 0.0  | 5.3  | 6.0  | 15.3 | 12.6 | 11.3 | 8.7  | 10.2 | 7.2  | 14.8 | 16.6 | 13.9 | 15.1 | 17.4 | 15.7 | 11.3 | 13.3 |
| 4                | 10.5 | 13.3 | 5.3  | 0.0  | 3.8  | 11.0 | 10.4 | 10.7 | 8.3  | 11.4 | 9.6  | 16.1 | 17.0 | 16.8 | 18.1 | 19.6 | 16.8 | 13.3 | 13.9 |
| 5                | 9.0  | 12.4 | 6.0  | 3.8  | 0.0  | 11.8 | 11.1 | 10.8 | 9.6  | 12.5 | 11.6 | 15.5 | 15.2 | 15.4 | 15.9 | 17.3 | 13.8 | 10.1 | 10.3 |
| 6                | 19.8 | 21.3 | 15.3 | 11.0 | 11.8 | 0.0  | 6.4  | 9.9  | 10.2 | 13.6 | 15.5 | 16.2 | 15.8 | 20.0 | 22.2 | 21.8 | 18.7 | 18.5 | 18.0 |
| 7                | 16.6 | 16.8 | 12.6 | 10.4 | 11.1 | 6.4  | 0.0  | 3.8  | 5.0  | 7.8  | 11.0 | 10.1 | 11.1 | 14.3 | 17.4 | 17.0 | 15.3 | 15.3 | 15.9 |
| 8                | 14.3 | 13.7 | 11.3 | 10.7 | 10.8 | 9.9  | 3.8  | 0.0  | 3.8  | 5.4  | 9.3  | 6.6  | 8.6  | 10.5 | 13.9 | 13.7 | 12.9 | 12.8 | 14.1 |
| 9                | 13.0 | 12.7 | 8.7  | 8.3  | 9.6  | 10.2 | 5.0  | 3.8  | 0.0  | 3.8  | 6.0  | 9.2  | 12.1 | 12.1 | 15.4 | 16.1 | 15.3 | 13.8 | 15.4 |
| 10               | 13.5 | 11.9 | 10.2 | 11.4 | 12.5 | 13.6 | 7.8  | 5.4  | 3.8  | 0.0  | 5.0  | 7.8  | 12.4 | 10.5 | 14.6 | 15.5 | 16.0 | 14.7 | 17.0 |
| 11               | 11.2 | 10.2 | 7.2  | 9.6  | 11.6 | 15.5 | 11.0 | 9.3  | 6.0  | 5.0  | 0.0  | 12.0 | 16.2 | 12.8 | 16.1 | 18.0 | 18.2 | 15.3 | 17.8 |
| 12               | 15.6 | 13.1 | 14.8 | 16.1 | 15.5 | 16.2 | 10.1 | 6.6  | 9.2  | 7.8  | 12.0 | 0.0  | 6.0  | 5.9  | 10.2 | 9.5  | 11.4 | 12.8 | 14.9 |
| 13               | 16.7 | 15.4 | 16.6 | 17.0 | 15.2 | 15.8 | 11.1 | 8.6  | 12.1 | 12.4 | 16.2 | 6.0  | 0.0  | 8.2  | 9.8  | 7.4  | 7.3  | 11.0 | 11.7 |
| 14               | 12.5 | 9.2  | 13.9 | 16.8 | 15.4 | 20.0 | 14.3 | 10.5 | 12.1 | 10.5 | 12.8 | 5.9  | 8.2  | 0.0  | 5.0  | 6.0  | 9.5  | 9.7  | 12.8 |
| 15               | 11.8 | 9.4  | 15.1 | 18.1 | 15.9 | 22.2 | 17.4 | 13.9 | 15.4 | 14.6 | 16.1 | 10.2 | 9.8  | 5.0  | 0.0  | 3.8  | 7.1  | 7.2  | 10.2 |
| 16               | 15.0 | 12.8 | 17.4 | 19.6 | 17.3 | 21.8 | 17.0 | 13.7 | 16.1 | 15.5 | 18.0 | 9.5  | 7.4  | 6.0  | 3.8  | 0.0  | 5.6  | 8.8  | 10.8 |
| 17               | 13.7 | 13.6 | 15.7 | 16.8 | 13.8 | 18.7 | 15.3 | 12.9 | 15.3 | 16.0 | 18.2 | 11.4 | 7.3  | 9.5  | 7.1  | 5.8  | 0.0  | 5.7  | 5.7  |
| 18               | 8.3  | 9.3  | 11.3 | 13.3 | 10.1 | 18.5 | 15.3 | 12.8 | 13.8 | 14.7 | 15.3 | 12.8 | 11.0 | 9.7  | 7.2  | 8.8  | 5.7  | 0.0  | 3.8  |
| 19               | 11.0 | 12.9 | 13.3 | 13.9 | 10.3 | 18.0 | 15.9 | 14.1 | 15.4 | 17.0 | 17.8 | 14.9 | 11.7 | 12.8 | 10.2 | 10.8 | 5.7  | 3.8  | 0.0  |

the center point of each said  $\alpha$ -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center points of each said sphere having the following structural coordinates:

| $\alpha$ -Carbon Number | X Position | Y Position | Z Position |
|-------------------------|------------|------------|------------|
| 1                       | 119.144    | 43.487     | 44.133     |
| 2                       | 120.203    | 38.695     | 43.506     |
| 3                       | 114.058    | 43.884     | 41.015     |
| 4                       | 109.327    | 46.145     | 41.743     |
| 5                       | 110.682    | 46.410     | 45.284     |
| 6                       | 99.381     | 42.920     | 45.148     |
| 7                       | 103.445    | 38.054     | 44.605     |
| 8                       | 106.807    | 36.336     | 45.151     |
| 9                       | 107.629    | 38.010     | 41.804     |
| 10                      | 109.375    | 34.842     | 40.617     |
| 11                      | 111.944    | 37.854     | 37.602     |
| 12                      | 110.233    | 31.098     | 47.361     |
| 13                      | 109.178    | 33.314     | 52.875     |
| 14                      | 115.915    | 32.218     | 48.369     |
| 15                      | 118.846    | 34.443     | 51.796     |
| 16                      | 116.461    | 32.848     | 54.290     |
| 17                      | 114.100    | 38.006     | 55.620     |
| 18                      | 116.617    | 41.285     | 51.702     |
| 19                      | 114.855    | 43.486     | 54.238     |

, each said  $\alpha$ -carbon having an associated R-group, said synthase having an ordered arrangement of said R-groups other than the following ordered arrangements of R-groups:

Table 7

| Ordered Arrangement of R-Groups at $\alpha$ -carbons 1-19 |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |
|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|
|   | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |
| A   | C | W | I | I | S | Y | T | T | T | Y  | L  | C  | D  | V  | T  | Y  | D  | Y  | T  |
| B   | C | W | I | I | S | Y | T | S | T | Y  | L  | C  | D  | I  | T  | Y  | D  | Y  | Y  |
| C   | G | W | I | A | S | Y | T | C | G | Y  | L  | C  | D  | M  | L  | Y  | D  | Y  | Y  |
| D   | G | W | I | A | S | Y | T | S | G | Y  | L  | C  | D  | M  | L  | Y  | D  | Y  | Y  |
| E   | C | W | L | T | S | Y | S | A | G | Y  | I  | A  | N  | A  | V  | Y  | D  | Y  | Y  |
| F   | G | W | L | L | S | Y | S | T | V | H  | L  | G  | D  | A  | L  | Y  | D  | Y  | Y  |
| G   | C | W | L | T | S | Y | S | A | G | Y  | I  | A  | N  | A  | L  | Y  | D  | Y  | Y  |
| H   | L | W | I | T | T | Y | S | V | G | N  | L  | F  | D  | V  | L  | Y  | D  | Y  | Y  |
| I   | P | W | I | V | D | Y | S | T | A | G  | L  | S  | D  | A  | C  | Y  | D  | Y  | Y  |
| J   | A | W | V | C | G | F | T | S | C | I  | M  | G  | N  | C  | S  | Y  | D  | Y  | Y  |
| K   | N | F | F | L | G | A | E | I | T | A  | T  | G  | N  | I  | T  | Y  | D  | Y  | Y  |
| L   | C | W | N | I | T | Y | S | I | S | G  | M  | L  | D  | A  | M  | Y  | D  | Y  | Y  |
| M   | S | W | V | L | T | Y | S | S | S | Y  | L  | G  | G  | V  | L  | Y  | D  | Y  | Y  |
| N   | N | F | F | L | V | N | A | T | L | A  | L  | G  | N  | L  | S  | Y  | D  | Y  | Y  |
| O   | C | W | N | I | T | Y | I | S | G | P  | L  | L  | D  | A  | M  | Y  | D  | Y  | Y  |
| P   | C | W | N | V | T | Y | I | G | G | I  | L  | L  | D  | A  | M  | Y  | D  | Y  | Y  |
| Q   | C | Y | L | L | T | F | A | V | T | M  | T  | G  | N  | I  | T  | Y  | D  | Y  | Y  |
| R   | C | W | I | I | T | Y | S | I | S | A  | I  | L  | D  | A  | I  | Y  | D  | Y  | Y  |
| S   | S | W | F | I | V | F | S | S | S | V  | I  | L  | N  | V  | I  | Y  | D  | Y  | Y  |
| T   | S | W | I | A | T | Y | S | V | A | S  | I  | L  | D  | A  | I  | Y  | D  | Y  | Y  |
| U   | N | W | N | L | T | Y | S | I | S | S  | I  | F  | N  | S  | M  | Y  | D  | Y  | Y  |
| V   | F | L | A | Q | T | Y | S | I | G | Q  | L  | S  | D  | T  | I  | F  | Y  | Y  | Y  |
| W   | I | S | S | T | V | Y | S | I | A | L  | V  | G  | N  | M  | F  | Y  | Y  | Y  | Y  |
| X   | Y | L | C | I | T | Y | S | C | G | H  | S  | L  | G  | F  | G  | Y  | Y  | Y  | Y  |
| Y   | G | S | F | I | T | F | S | S | S | V  | I  | L  | N  | A  | V  | Y  | Y  | Y  | Y  |
| Z   | Y | W | A | C | T | Y | S | S | G | M  | L  | G  | D  | L  | I  | Y  | Y  | Y  | Y  |

Table 7

|    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AA | A | A | A | N | L | T | S | T | C | M | L | L | L | Y | D | Y | N |
| BB | F | L | C | C | V | T | Y | V | L | G | S | L | L | F | D | F | S |
| CC | F | W | A | A | M | T | Y | L | S | D | T | M | V | Y | D | F | S |
| DD | Y | M | C | C | V | T | F | I | L | G | S | V | F | Y | D | Y | T |
| EE | V | S | G | G | Q | V | Y | C | W | N | G | A | V | Y | D | Y | G |
| FF | C | S | G | G | T | T | M | V | G | N | L | F | L | Y | D | F | T |
| GG | C | S | G | G | T | T | M | I | G | N | L | F | L | Y | D | F | T |
| HH | C | A | G | G | T | T | M | I | G | N | L | F | L | Y | D | F | T |
| II | I | W | V | V | I | S | Y | V | I | N | L | V | T | Y | D | Y | T |
| JJ | Y | W | A | A | C | T | Y | L | G | D | L | L | L | Y | D | Y | T |
| KK | C | W | I | I | I | S | Y | L | C | D | L | V | I | Y | D | Y | T |
| LL | C | W | I | I | I | S | Y | L | C | D | L | V | I | Y | D | Y | T |
| MM | C | W | N | N | I | T | Y | M | L | D | L | A | M | Y | D | F | G |
| NN | F | A | A | A | Q | T | Y | Q | S | D | L | T | I | Y | D | F | G |
| OO | F | A | I | I | A | T | Y | S | L | D | L | A | I | Y | D | F | G |

89. The synthase of claim 88, wherein said synthase has 25% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2.
90. The synthase of claim 88, wherein said synthase has 35% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2.
91. The synthase of claim 88, wherein said synthase catalyses the formation of a terpenoid product from a monoterpene substrate.
92. The synthase of claim 88, wherein said synthase catalyses the formation of a terpenoid product from a sesquiterpene substrate.
93. The synthase of claim 88, wherein said synthase catalyses the formation of a terpenoid product from a diterpene substrate.
94. The synthase of claims 91, 92, or 93; wherein said product is a cyclic terpenoid hydrocarbon.
95. A isolated protein comprising:
  - a first domain having an amino terminal end and a carboxyl terminal end; said first domain comprising amino acids that align structurally in three-dimensional space with a glycosyl hydrolase catalytic core, said glycosyl hydrolase catalytic core selected from the group consisting of amino acids 36 to 230 of glucoamylase PDB code 3GLY of *Aspergillus awamori* and amino acids 36 to 230 of endoglucanase CelD PDB code 1CLC;
  - a second domain having an amino terminal end and carboxyl terminal end, said second domain comprising amino acids that align structurally in three-dimensional space with avian FPP synthase, said carboxyl terminal end of said first domain linked to said amino terminal end of said second domain; wherein a region of said second domain has 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, and wherein said second domain comprises nine  $\alpha$ -carbons having interatomic distances in Angstroms between said  $\alpha$ -carbons that are  $\pm 2.3$  Angstroms of the following interatomic distances:

| $\alpha$ -Carbon | 1    | 2    | 3    | 4    | 5    | 6    | 7    | 8    | 9    |
|------------------|------|------|------|------|------|------|------|------|------|
| 1                | 0.0  | 8.4  | 13.7 | 12.7 | 11.9 | 10.2 | 13.1 | 9.4  | 12.8 |
| 2                | 8.4  | 0.0  | 11.3 | 8.7  | 10.2 | 7.2  | 14.8 | 15.1 | 17.4 |
| 3                | 13.7 | 11.3 | 0.0  | 3.8  | 5.4  | 9.3  | 6.6  | 13.9 | 13.7 |
| 4                | 12.7 | 8.7  | 3.8  | 0.0  | 3.8  | 6.0  | 9.2  | 15.4 | 16.1 |
| 5                | 11.9 | 10.2 | 5.4  | 3.8  | 0.0  | 5.0  | 7.8  | 14.6 | 15.5 |
| 6                | 10.2 | 7.2  | 9.3  | 6.0  | 5.0  | 0.0  | 12.0 | 16.1 | 18.0 |
| 7                | 13.1 | 14.8 | 6.6  | 9.2  | 7.8  | 12.0 | 0.0  | 10.2 | 9.5  |
| 8                | 9.4  | 15.1 | 13.9 | 15.4 | 14.6 | 16.1 | 10.2 | 0.0  | 3.8  |
| 9                | 12.8 | 17.4 | 13.7 | 16.1 | 15.5 | 18.0 | 9.5  | 3.8  | 0.0  |

the center point of each said  $\alpha$ -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center point of each said sphere having the following structural coordinates:

| $\alpha$ -Carbon Number | X Position | Y Position | Z Position |
|-------------------------|------------|------------|------------|
| 1                       | 120.203    | 38.695     | 43.506     |
| 2                       | 114.058    | 43.884     | 41.015     |
| 3                       | 106.807    | 36.336     | 45.151     |
| 4                       | 107.629    | 38.010     | 41.804     |
| 5                       | 109.375    | 34.842     | 40.617     |
| 6                       | 111.944    | 37.854     | 37.602     |
| 7                       | 110.233    | 31.098     | 47.361     |
| 8                       | 118.846    | 34.443     | 51.796     |
| 9                       | 116.461    | 32.848     | 54.290     |

, each said  $\alpha$ -carbon having an associated R-group, said synthase having an ordered arrangement of R-groups other than the following ordered arrangements of R-groups:

Table 9

| Ordered Arrangements of $\alpha$ -Carbons 1-9 |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|
|   | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
| A   | W | I | T | T | Y | L | C | T | Y |
| B   | W | I | S | T | Y | L | C | T | Y |
| C   | W | I | C | G | Y | L | C | L | Y |
| D   | W | I | S | G | Y | L | C | L | Y |
| E   | W | L | A | G | Y | I | A | L | Y |
| F   | W | L | T | V | H | L | G | V | Y |
| G   | W | L | A | G | Y | I | A | L | Y |
| H   | W | I | V | G | N | L | F | L | Y |
| I   | W | I | T | A | G | L | S | C | Y |
| J   | W | V | S | C | I | M | G | S | Y |
| K   | F | F | I | T | A | T | G | T | Y |
| L   | W | N | I | S | G | M | L | M | Y |
| M   | W | V | S | S | Y | L | G | L | Y |
| N   | F | F | T | L | A | L | G | S | Y |
| O   | W | N | S | G | P | L | L | M | Y |
| P   | W | N | G | G | I | L | L | I | Y |
| Q   | Y | L | V | T | M | T | G | T | Y |
| R   | W | I | I | S | A | I | L | I | Y |
| S   | W | F | S | S | V | I | L | I | Y |
| T   | W | I | V | A | S | I | L | I | Y |
| U   | W | N | I | S | S | I | F | M | Y |
| V   | L | A | I | G | Q | L | S | I | F |
| W   | S | S | I | A | L | V | G | F | Y |
| X   | L | C | C | G | H | S | L | G | Y |
| Y   | S | F | S | S | V | I | L | V | Y |
| Z   | W | A | S | G | M | L | G | I | Y |

Table 9

|    |   |   |   |   |   |   |   |   |   |
|----|---|---|---|---|---|---|---|---|---|
| AA | A | N | L | T | S | T | C | L | Y |
| BB | L | C | S | A | Y | V | L | L | Y |
| CC | W | A | T | G | M | L | S | M | Y |
| DD | M | C | S | S | G | I | L | V | Y |
| EE | S | G | V | G | L | C | W | F | Y |
| FF | S | G | A | L | G | V | G | F | Y |
| GG | S | G | F | A | L | I | G | F | Y |
| HH | A | G | F | A | L | I | G | F | Y |
| II | W | V | T | G | L | V | I | S | Y |
| JJ | W | A | S | G | M | L | G | I | Y |
| KK | W | I | S | T | Y | L | C | T | Y |
| LL | W | I | T | T | Y | L | C | T | Y |
| MM | W | N | I | S | G | M | L | M | Y |
| NN | A | A | I | G | Q | L | S | I | F |
| OO | A | I | V | A | S | I | L | I | Y |



96. The protein of claim 95, wherein said synthase has 25% or greater sequence identity to SEQ ID NO: 2.
97. The protein of claim 96, wherein said synthase has 35% or greater sequence identity to SEQ ID NO: 2.
98. The synthase of claim 95, wherein said synthase catalyses the formation of a terpenoid product from a monoterpene substrate.
99. The synthase of claim 95, wherein said synthase catalyses the formation of a terpenoid product from a sesquiterpene substrate.
100. The synthase of claim 95, wherein said synthase catalyses the formation of a terpenoid product from a diterpene substrate.
101. The synthase of claims 98, 99, or 100, wherein said product is a cyclic terpenoid hydrocarbon.
102. An isolated synthase having a region with 40% or greater sequence identity to residues 343 to 612 of SEQ ID NO: 20, wherein one or more amino acid residues of said synthase that align with amino acids at positions 348, 351, 372, 375, 376, 454, 479, 480, 481, 482, 485, 519, 523, 597, 600, 601, 605, 607 and 608 of SEQ ID NO: 20 are residues other than the following ordered arrangements of residues:

[illegible]

**claim 102**

|    |   | Ordered Arrangements of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|---|----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|    |   | 348                              | 351 | 372 | 375 | 376 | 454 | 479 | 480 | 481 | 482 | 485 | 519 | 523 | 597 | 600 | 601 | 605 | 607 | 608 |
| A  | C | W                                | I   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B  | G | W                                | I   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C  | G | W                                | I   | A   | S   | Y   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D  | G | W                                | L   | A   | S   | Y   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E  | C | W                                | L   | T   | S   | Y   | S   | A   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| F  | G | W                                | L   | L   | S   | Y   | S   | Y   | T   | V   | H   | L   | A   | D   | A   | V   | Y   | D   | Y   | T   |
| G  | C | W                                | L   | T   | S   | Y   | S   | A   | G   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | S   |
| H  | L | W                                | I   | T   | T   | Y   | S   | S   | V   | G   | N   | L   | F   | D   | V   | L   | Y   | D   | F   | T   |
| I  | P | W                                | I   | V   | D   | Y   | S   | T   | A   | G   | N   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |
| J  | A | W                                | V   | C   | G   | F   | T   | S   | T   | A   | G   | L   | S   | D   | C   | S   | Y   | D   | Y   | S   |
| K  | N | F                                | L   | L   | G   | A   | E   | I   | T   | T   | A   | T   | G   | N   | I   | T   | Y   | E   | F   | T   |
| L  | C | W                                | N   | I   | T   | Y   | S   | I   | S   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | Q   |
| M  | S | W                                | V   | L   | T   | Y   | S   | S   | S   | Y   | L   | G   | L   | D   | V   | L   | Y   | D   | F   | T   |
| N  | N | F                                | F   | L   | T   | N   | A   | T   | L   | A   | L   | L   | G   | N   | L   | S   | Y   | E   | F   | T   |
| O  | C | W                                | N   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | L   | D   | A   | M   | Y   | D   | H   | G   |
| P  | C | W                                | N   | V   | T   | Y   | I   | G   | G   | I   | L   | L   | L   | D   | A   | I   | Y   | D   | F   | T   |
| Q  | C | Y                                | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | T   | Y   | D   | G   | G   |
| R  | C | W                                | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | L   | D   | A   | I   | Y   | D   | D   | G   |
| S  | W | F                                | I   | I   | V   | F   | S   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | H   | G   |
| T  | S | W                                | I   | A   | T   | Y   | S   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | G   |
| U  | N | W                                | N   | A   | T   | Y   | S   | I   | S   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | G   |
| V  | F | L                                | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | L   | S   | D   | S   | M   | F   | D   | H   | G   |
| W  | I | S                                | A   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | N   | M   | F   | Y   | D   | L   | T   |
| X  | Y | L                                | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | G   | N   | F   | G   | Y   | D   | H   | T   |
| Y  | G | S                                | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | N   | A   | A   | V   | Y   | D   | L   | S   |
| Z  | Y | W                                | A   | C   | T   | Y   | S   | S   | S   | M   | L   | L   | G   | D   | L   | I   | Y   | D   | L   | Y   |
| AA | A | A                                | N   | L   | T   | T   | N   | A   | L   | T   | S   | T   | C   | M   | L   | L   | Y   | D   | L   | N   |
| BB | F | L                                | C   | V   | T   | T   | Y   | S   | A   | Y   | V   | L   | G   | L   | L   | L   | Y   | D   | F   | S   |
| CC | F | W                                | A   | M   | T   | T   | Y   | N   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | F   | S   |
| DD | Y | M                                | C   | V   | T   | F   | V   | S   | S   | G   | I   | L   | L   | G   | F   | V   | Y   | D   | Y   | T   |
| EE | V | S                                | G   | Q   | V   | Y   | Y   | S   | V   | G   | L   | C   | W   | N   | V   | F   | Y   | D   | Y   | T   |
| FF | C | S                                | G   | T   | T   | M   | F   | A   | L   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | F   | T   |
| GG | C | S                                | A   | T   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | F   | T   |
| HH | C | A                                | G   | T   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | F   | T   |
| II | I | W                                | V   | I   | S   | Y   | Y   | T   | T   | G   | L   | V   | I   | N   | T   | S   | Y   | D   | Y   | T   |
| JJ | Y | W                                | A   | C   | T   | Y   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | L   | Y   |
| KK | Y | W                                | I   | I   | S   | Y   | Y   | T   | T   | Y   | L   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| LL | C | W                                | I   | I   | S   | Y   | Y   | T   | T   | Y   | L   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| MM | C | W                                | N   | I   | T   | Y   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | G   |
| NN | F | A                                | A   | Q   | T   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | F   | G   |
| OO | F | A                                | A   | T   | T   | Y   | S   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | G   |

103. An isolated synthase having a region with 40% or greater sequence identity to residues 316 to 586 of SEQ ID NO: 22, wherein one or more amino acid residues of said synthase that align with amino acids at positions 321, 324, 345, 348, 349, 427, 452, 453, 454, 455, 458, 492, 496, 569, 572, 573, 577, 579 and 580 of SEQ ID NO: 22 are residues other than the following ordered arrangements of residues:

103290" 028E6B60

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104. An isolated synthase having a region with 40% or greater sequence identity to residues 352 to 622 of SEQ ID NO: 58, wherein one or more amino acid residues of said synthase that align with amino acids at positions 357, 360, 381, 384, 385, 463, 487, 488, 489, 490, 493, 528, 532, 606, 609, 610, 614, 616 and 617 of SEQ ID NO: 58 are residues other than the following ordered arrangements of residues:

02936660 06290 02936660

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 | 357 | 360 | 381 | 384 | 385 | 463 | 487 | 488 | 489 | 490 | 493 | 528 | 532 | 606 | 609 | 610 | 614 | 616 | 617 |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G   | W   | I   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| F                               | G   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | G   | D   | A   | V   | Y   | D   | Y   | T   |
| G                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | L   | Y   | D   | Y   | S   |
| H                               | L   | W   | I   | T   | T   | Y   | S   | V   | G   | Y   | L   | F   | D   | V   | L   | Y   | D   | F   | T   |
| I                               | P   | W   | I   | V   | D   | Y   | S   | T   | G   | N   | L   | A   | D   | A   | L   | Y   | D   | Y   | T   |
| J                               | A   | W   | V   | C   | G   | F   | T   | S   | A   | G   | I   | S   | N   | C   | S   | Y   | E   | F   | T   |
| K                               | N   | F   | F   | L   | G   | A   | E   | I   | T   | A   | T   | G   | N   | I   | T   | Y   | D   | Y   | S   |
| L                               | C   | W   | N   | I   | T   | Y   | S   | S   | G   | Y   | M   | L   | D   | A   | M   | Y   | D   | H   | T   |
| M                               | S   | W   | V   | L   | T   | Y   | S   | S   | Y   | L   | L   | G   | G   | V   | L   | Y   | D   | F   | T   |
| N                               | N   | F   | F   | L   | V   | N   | A   | T   | S   | A   | L   | L   | N   | L   | S   | Y   | D   | H   | Q   |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | A   | P   | L   | L   | G   | L   | S   | Y   | E   | F   | T   |
| P                               | C   | W   | N   | V   | T   | Y   | I   | S   | G   | I   | L   | L   | L   | A   | M   | Y   | D   | H   | G   |
| Q                               | C   | Y   | L   | L   | T   | F   | A   | T   | G   | T   | T   | L   | D   | A   | I   | Y   | D   | F   | T   |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | N   | I   | T   | Y   | D   | Y   | G   |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | D   | A   | I   | Y   | D   | D   | G   |
| T                               | S   | W   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | N   | V   | I   | Y   | D   | H   | G   |
| U                               | N   | W   | N   | L   | T   | Y   | S   | S   | S   | I   | L   | F   | D   | A   | I   | Y   | D   | F   | G   |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | S   | Q   | L   | S   | N   | S   | M   | Y   | D   | H   | G   |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | T   | I   | F   | D   | F   | T   |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | I   | A   | L   | S   | L   | G   | M   | F   | Y   | D   | L   | G   |
| Y                               | G   | S   | F   | I   | T   | F   | S   | C   | G   | H   | S   | L   | N   | A   | G   | Y   | D   | Y   | S   |
| Z                               | Y   | W   | A   | C   | T   | Y   | S   | S   | S   | V   | I   | L   | N   | A   | V   | Y   | D   | H   | G   |
| AA                              | A   | A   | N   | L   | T   | N   | A   | S   | M   | L   | L   | G   | D   | L   | I   | Y   | D   | L   | Y   |
| BB                              | F   | L   | C   | V   | T   | Y   | A   | T   | S   | Y   | V   | C   | M   | L   | L   | Y   | D   | L   | Y   |
| CC                              | F   | W   | A   | M   | T   | Y   | S   | A   | Y   | L   | L   | S   | G   | L   | L   | Y   | D   | F   | N   |
| DD                              | Y   | M   | C   | V   | T   | F   | V   | G   | M   | L   | L   | S   | D   | I   | M   | Y   | D   | F   | S   |
| EE                              | V   | S   | G   | Q   | V   | Y   | S   | S   | G   | L   | C   | W   | N   | V   | F   | Y   | D   | Y   | T   |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | Y   | G   |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | F   | T   |
| HH                              | C   | A   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | F   | T   |
| II                              | I   | W   | V   | I   | S   | Y   | T   | G   | L   | L   | V   | I   | N   | T   | S   | Y   | D   | Y   | T   |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | G   | M   | L   | L   | G   | D   | L   | I   | Y   | D   | L   | Y   |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | T   | Y   | L   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | T   | Y   | L   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| MM                              | C   | W   | N   | I   | I   | T   | Y   | S   | I   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | G   |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | F   | G   |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | L   | L   | D   | A   | I   | Y   | D   | F   | G   |

105. An isolated synthase having a region with 40% or greater sequence identity to amino acid residues 272 to 540 encoded by SEQ ID NO: 33, wherein one or more amino acid residues of said synthase that align with amino acids at positions 277, 280, 301, 304, 305, 383, 408, 409, 410, 411, 414, 448, 452, 524, 527, 528, 532, 534 and 535 encoded by SEQ ID NO: 33 are residues other than the following ordered arrangements of residues:

102290 "028E6860

| Ordered Arrangement of Residues |   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 |   | 277 | 280 | 301 | 304 | 305 | 383 | 408 | 409 | 410 | 414 | 448 | 452 | 524 | 527 | 532 | 534 | 535 | 616 | 617 |
| A                               | C | W   | I   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C | W   | I   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G | W   | I   | A   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G | W   | I   | A   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E                               | C | W   | L   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | V   | Y   | D   | Y   | T   |
| F                               | G | W   | L   | L   | T   | S   | Y   | S   | T   | V   | H   | L   | G   | N   | A   | V   | Y   | D   | Y   | T   |
| G                               | C | W   | L   | T   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| H                               | L | W   | I   | T   | T   | T   | Y   | S   | V   | G   | N   | L   | F   | D   | V   | L   | Y   | D   | Y   | T   |
| I                               | P | W   | I   | V   | C   | D   | Y   | S   | T   | A   | G   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |
| J                               | A | W   | V   | V   | C   | G   | F   | T   | T   | A   | I   | M   | G   | N   | I   | S   | Y   | D   | Y   | T   |
| K                               | N | F   | F   | L   | L   | G   | A   | E   | I   | T   | A   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| L                               | C | W   | N   | I   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | G   | V   | L   | Y   | D   | Y   | T   |
| M                               | S | W   | V   | L   | L   | T   | Y   | S   | S   | S   | Y   | L   | G   | N   | L   | S   | Y   | D   | Y   | T   |
| N                               | N | F   | F   | L   | L   | V   | N   | A   | T   | L   | A   | L   | G   | N   | L   | S   | Y   | D   | Y   | T   |
| O                               | C | W   | N   | I   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| P                               | C | W   | N   | V   | V   | T   | Y   | I   | G   | I   | L   | L   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| Q                               | C | Y   | L   | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |
| R                               | C | W   | I   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| S                               | S | W   | F   | I   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | Y   | T   |
| T                               | S | W   | I   | A   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| U                               | N | W   | N   | L   | L   | T   | Y   | S   | I   | S   | S   | I   | F   | N   | S   | M   | Y   | D   | Y   | T   |
| V                               | F | L   | A   | Q   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | Y   | T   |
| W                               | I | S   | S   | T   | V   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | M   | F   | Y   | D   | Y   | T   |
| X                               | Y | L   | C   | I   | T   | T   | Y   | S   | C   | G   | H   | S   | L   | G   | A   | G   | Y   | D   | Y   | T   |
| Y                               | G | S   | F   | I   | I   | T   | F   | S   | S   | V   | V   | I   | L   | N   | L   | V   | Y   | D   | Y   | T   |
| Z                               | Y | W   | A   | C   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |
| AA                              | A | A   | N   | L   | L   | T   | N   | A   | L   | T   | S   | T   | C   | M   | L   | L   | Y   | D   | Y   | T   |
| BB                              | F | L   | C   | V   | V   | T   | Y   | S   | A   | Y   | V   | L   | S   | G   | L   | L   | Y   | D   | Y   | T   |
| CC                              | F | W   | A   | M   | M   | T   | Y   | N   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | Y   | T   |
| DD                              | Y | M   | C   | V   | V   | T   | Y   | V   | S   | S   | G   | I   | L   | G   | F   | V   | Y   | D   | Y   | T   |
| EE                              | V | S   | G   | Q   | Q   | V   | Y   | S   | V   | G   | L   | C   | W   | N   | V   | F   | Y   | D   | Y   | T   |
| FF                              | C | S   | G   | T   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| GG                              | C | S   | G   | T   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| HH                              | C | A   | G   | T   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| II                              | I | W   | V   | I   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | T   | S   | Y   | D   | Y   | T   |
| JJ                              | Y | W   | A   | C   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |
| KK                              | C | W   | I   | I   | I   | S   | Y   | T   | T   | Y   | L   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| LL                              | C | W   | I   | I   | I   | S   | Y   | T   | T   | Y   | L   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| MM                              | C | W   | N   | I   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| NN                              | F | A   | A   | Q   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | Y   | T   |
| OO                              | F | A   | I   | A   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |



106. An isolated synthase having a region with 40% or greater sequence identity to residues 319 to 571 of SEQ ID NO: 42, wherein one or more amino acid residues of said synthase that align with amino acids at positions 324, 327, 348, 351, 352, 430, 455, 456, 457, 458, 461, 495, 499, 571, 574, 575, 579, 581 and 582 of SEQ ID NO: 42 are residues other than the following ordered arrangements of residues:

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 | 324 | 327 | 348 | 351 | 352 | 430 | 455 | 456 | 457 | 458 | 461 | 495 | 499 | 571 | 574 | 575 | 579 | 581 | 582 |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G   | W   | I   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| F                               | G   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | G   | D   | A   | V   | Y   | D   | Y   | T   |
| G                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| H                               | L   | W   | I   | T   | T   | Y   | S   | V   | G   | N   | L   | F   | D   | V   | L   | Y   | D   | Y   | T   |
| I                               | P   | W   | I   | V   | D   | Y   | S   | T   | A   | G   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |
| J                               | A   | W   | V   | C   | G   | F   | T   | S   | C   | I   | M   | G   | N   | C   | S   | Y   | D   | Y   | T   |
| K                               | N   | F   | F   | L   | G   | A   | E   | I   | T   | A   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |
| L                               | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| M                               | S   | W   | V   | L   | T   | Y   | S   | S   | S   | Y   | L   | G   | G   | V   | L   | Y   | D   | Y   | T   |
| N                               | N   | F   | F   | L   | V   | N   | A   | T   | L   | A   | L   | G   | N   | L   | S   | Y   | D   | Y   | T   |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| P                               | C   | W   | N   | V   | T   | Y   | I   | G   | I   | L   | L   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| Q                               | C   | Y   | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | Y   | T   |
| T                               | S   | W   | I   | A   | T   | Y   | S   | S   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| U                               | N   | W   | N   | L   | T   | Y   | S   | I   | S   | S   | I   | F   | N   | S   | M   | Y   | D   | Y   | T   |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | L   | D   | T   | I   | F   | D   | Y   | T   |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | M   | F   | Y   | D   | Y   | T   |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | G   | F   | G   | Y   | D   | Y   | T   |
| Y                               | G   | S   | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | N   | A   | V   | Y   | D   | Y   | T   |
| Z                               | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |
| AA                              | A   | A   | N   | L   | T   | N   | A   | S   | T   | S   | T   | C   | M   | L   | L   | Y   | D   | Y   | T   |
| BB                              | F   | L   | C   | V   | T   | Y   | S   | S   | A   | Y   | V   | L   | G   | L   | L   | Y   | D   | Y   | T   |
| CC                              | F   | W   | A   | M   | T   | Y   | N   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | Y   | T   |
| DD                              | Y   | M   | C   | V   | T   | F   | V   | S   | S   | G   | I   | L   | G   | F   | V   | Y   | D   | Y   | T   |
| EE                              | V   | S   | G   | Q   | V   | Y   | S   | V   | G   | L   | C   | W   | N   | V   | F   | Y   | D   | Y   | T   |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| HH                              | C   | A   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | Y   | T   |
| II                              | I   | W   | V   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | T   | S   | Y   | D   | Y   | T   |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| MM                              | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | I   | T   | Y   | D   | Y   | T   |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | A   | M   | Y   | D   | Y   | T   |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |

107. An isolated synthase having a region with 40% or greater sequence identity to residues 579 to 847 of SEQ ID NO: 44, wherein one or more amino acid residues of said synthase that align with amino acids at positions 584, 587, 606, 609, 610, 688, 713, 714, 715, 716, 719, 753, 757, 831, 834, 835, 839, 841 and 842 of SEQ ID NO: 44 are residues other than the following ordered arrangements of residues:

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|                                 | 584 | 587 | 606 | 609 | 610 | 688 | 713 | 714 | 715 | 716 | 719 | 753 | 757 | 831 | 834 | 835 | 839 | 841 | 842 |  |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |  |
| B                               | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |  |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |  |
| D                               | G   | W   | I   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |  |
| E                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |  |
| F                               | G   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | G   | N   | A   | V   | Y   | D   | Y   | T   |  |
| G                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |  |
| H                               | L   | W   | I   | T   | T   | Y   | S   | V   | G   | N   | L   | F   | D   | V   | L   | Y   | D   | Y   | T   |  |
| I                               | P   | W   | I   | V   | D   | Y   | S   | T   | A   | G   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |  |
| J                               | A   | W   | V   | C   | G   | F   | T   | S   | C   | I   | M   | G   | N   | C   | S   | Y   | D   | Y   | T   |  |
| K                               | N   | F   | F   | L   | G   | A   | E   | I   | T   | A   | M   | G   | N   | I   | T   | Y   | D   | Y   | T   |  |
| L                               | C   | W   | N   | I   | T   | Y   | S   | S   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |  |
| M                               | S   | W   | V   | L   | T   | Y   | S   | S   | Y   | L   | L   | G   | G   | V   | L   | Y   | D   | Y   | T   |  |
| N                               | N   | F   | F   | L   | V   | N   | A   | T   | L   | A   | L   | G   | N   | L   | S   | Y   | D   | Y   | T   |  |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | M   | Y   | D   | Y   | T   |  |
| P                               | C   | W   | N   | V   | T   | Y   | I   | G   | G   | I   | L   | L   | D   | A   | I   | Y   | D   | Y   | T   |  |
| Q                               | C   | Y   | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |  |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |  |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | Y   | T   |  |
| T                               | S   | W   | I   | A   | T   | Y   | S   | S   | A   | S   | I   | L   | N   | A   | I   | Y   | D   | Y   | T   |  |
| U                               | N   | W   | N   | L   | T   | Y   | S   | I   | S   | S   | I   | F   | N   | S   | M   | Y   | D   | Y   | T   |  |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | Y   | T   |  |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | M   | F   | Y   | D   | Y   | T   |  |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | G   | F   | G   | Y   | D   | Y   | T   |  |
| Y                               | G   | S   | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | N   | A   | V   | Y   | D   | Y   | T   |  |
| Z                               | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |  |
| AA                              | A   | A   | N   | L   | T   | N   | A   | L   | T   | S   | T   | C   | M   | L   | L   | Y   | D   | Y   | T   |  |
| BB                              | F   | L   | C   | V   | T   | Y   | S   | S   | A   | Y   | V   | L   | G   | L   | L   | Y   | D   | Y   | T   |  |
| CC                              | F   | W   | A   | M   | T   | Y   | N   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | Y   | T   |  |
| DD                              | Y   | M   | C   | V   | T   | F   | V   | S   | S   | G   | I   | L   | G   | F   | V   | Y   | D   | Y   | T   |  |
| EE                              | V   | S   | G   | Q   | V   | Y   | S   | V   | G   | L   | C   | W   | N   | V   | F   | Y   | D   | Y   | T   |  |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | Y   | T   |  |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | Y   | T   |  |
| HH                              | C   | A   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | Y   | T   |  |
| II                              | I   | W   | V   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | T   | S   | Y   | D   | Y   | T   |  |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |  |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |  |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |  |
| MM                              | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |  |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | Y   | T   |  |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |  |

108. An isolated synthase having a region with 40% or greater sequence identity to residues 495 to 767 of SEQ ID NO: 46, wherein one or more amino acid residues of said synthase that align with amino acids at positions 500, 503, 524, 527, 528, 606, 631, 632, 633, 634, 637, 674, 678, 751, 754, 755, 759, 761 and 762 of SEQ ID NO: 46 are residues other than the following ordered arrangements of residues:

|    |   | Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|----|---|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|    |   | 500                             | 503 | 524 | 527 | 528 | 606 | 631 | 632 | 633 | 634 | 637 | 674 | 678 | 751 | 754 | 755 | 759 | 761 | 762 |  |  |
| A  | C | W                               | I   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |  |  |
| B  | C | W                               | I   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |  |  |
| C  | G | W                               | I   | A   | S   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |  |  |
| D  | G | W                               | I   | A   | S   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |  |  |
| E  | C | W                               | L   | T   | S   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |  |  |
| F  | G | W                               | L   | L   | S   | S   | Y   | S   | T   | V   | H   | L   | G   | D   | A   | V   | Y   | D   | Y   | T   |  |  |
| G  | C | W                               | L   | T   | S   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |  |  |
| H  | L | W                               | I   | T   | T   | T   | Y   | S   | V   | G   | N   | L   | F   | D   | V   | L   | Y   | D   | Y   | T   |  |  |
| I  | P | W                               | I   | V   | D   | T   | Y   | S   | T   | A   | G   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |  |  |
| J  | A | W                               | V   | C   | G   | G   | F   | T   | S   | C   | I   | M   | G   | N   | C   | S   | Y   | D   | Y   | T   |  |  |
| K  | N | F                               | F   | L   | L   | T   | A   | E   | I   | T   | A   | T   | G   | N   | I   | T   | Y   | E   | F   | T   |  |  |
| L  | C | W                               | N   | I   | T   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | Q   |  |  |
| M  | S | W                               | V   | L   | T   | T   | Y   | S   | S   | S   | Y   | L   | G   | G   | V   | L   | Y   | D   | F   | T   |  |  |
| N  | N | F                               | F   | L   | V   | T   | Y   | A   | T   | L   | A   | L   | G   | N   | L   | S   | Y   | D   | F   | T   |  |  |
| O  | C | W                               | N   | I   | T   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | M   | Y   | D   | H   | G   |  |  |
| P  | C | W                               | N   | V   | T   | T   | Y   | I   | G   | G   | I   | L   | L   | D   | A   | I   | Y   | D   | F   | G   |  |  |
| Q  | C | Y                               | L   | L   | T   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |  |  |
| R  | C | W                               | I   | I   | T   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | H   | G   |  |  |
| S  | S | W                               | F   | I   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | F   | G   |  |  |
| T  | S | W                               | I   | A   | T   | T   | Y   | S   | S   | S   | S   | I   | L   | D   | A   | I   | Y   | D   | H   | G   |  |  |
| U  | N | W                               | N   | L   | T   | T   | Y   | S   | I   | A   | S   | I   | L   | N   | A   | M   | Y   | D   | F   | G   |  |  |
| V  | F | L                               | A   | Q   | T   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | S   | I   | F   | D   | H   | G   |  |  |
| W  | I | S                               | S   | T   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | T   | M   | Y   | D   | L   | T   |  |  |
| X  | Y | L                               | C   | I   | T   | T   | Y   | S   | C   | G   | H   | S   | L   | G   | F   | G   | Y   | D   | Y   | S   |  |  |
| Y  | G | S                               | F   | I   | T   | T   | Y   | S   | S   | S   | V   | I   | L   | N   | A   | V   | Y   | D   | H   | G   |  |  |
| Z  | Y | W                               | A   | C   | T   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | L   | Y   | D   | L   | Y   |  |  |
| AA | A | A                               | N   | L   | T   | T   | Y   | A   | L   | T   | S   | V   | C   | M   | L   | L   | Y   | D   | Y   | N   |  |  |
| BB | F | L                               | C   | V   | T   | T   | Y   | S   | T   | A   | Y   | T   | L   | G   | L   | L   | Y   | D   | F   | S   |  |  |
| CC | F | W                               | A   | M   | T   | T   | Y   | S   | S   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | F   | S   |  |  |
| DD | Y | M                               | C   | V   | T   | T   | Y   | S   | S   | G   | L   | C   | W   | N   | V   | F   | Y   | D   | Y   | T   |  |  |
| EE | V | S                               | G   | Q   | V   | V   | Y   | S   | V   | G   | L   | V   | G   | N   | L   | F   | Y   | D   | Y   | G   |  |  |
| FF | C | S                               | G   | T   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | F   | T   |  |  |
| GG | C | S                               | G   | T   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | Y   | T   |  |  |
| HH | C | A                               | G   | T   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | Y   | T   |  |  |
| II | I | W                               | V   | I   | S   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | T   | S   | Y   | D   | L   | Y   |  |  |
| JJ | Y | W                               | A   | C   | T   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | T   | Y   | D   | Y   | T   |  |  |
| KK | C | W                               | I   | I   | S   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |  |  |
| LL | C | W                               | I   | I   | S   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |  |  |
| MM | C | W                               | N   | I   | T   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | G   |  |  |
| NN | F | A                               | A   | Q   | T   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | F   | G   |  |  |
| OO | F | A                               | I   | A   | T   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | G   |  |  |



| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 | 300 | 303 | 324 | 327 | 328 | 408 | 431 | 432 | 433 | 434 | 437 | 471 | 475 | 548 | 551 | 552 | 556 | 558 | 559 |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C   | W   | I   | I   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G   | W   | I   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| F                               | G   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | G   | D   | A   | V   | Y   | D   | Y   | T   |
| G                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| H                               | L   | W   | I   | T   | S   | Y   | S   | V   | G   | Y   | L   | F   | D   | V   | L   | Y   | D   | Y   | T   |
| I                               | P   | W   | I   | V   | D   | Y   | S   | T   | A   | G   | L   | G   | D   | A   | C   | Y   | D   | Y   | T   |
| J                               | A   | W   | V   | C   | G   | F   | T   | S   | C   | I   | M   | G   | N   | C   | S   | Y   | D   | Y   | T   |
| K                               | N   | F   | F   | L   | G   | A   | E   | I   | T   | A   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |
| L                               | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| M                               | S   | W   | V   | L   | T   | Y   | S   | S   | L   | Y   | L   | G   | N   | V   | L   | Y   | D   | Y   | T   |
| N                               | N   | F   | F   | L   | V   | N   | A   | T   | L   | A   | L   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| P                               | C   | W   | N   | V   | T   | Y   | I   | G   | G   | I   | L   | L   | D   | A   | T   | Y   | D   | Y   | T   |
| Q                               | C   | Y   | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | Y   | T   |
| T                               | S   | W   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| U                               | N   | W   | N   | L   | T   | Y   | S   | I   | S   | S   | I   | F   | N   | S   | M   | Y   | D   | Y   | T   |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | Y   | T   |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | M   | F   | Y   | D   | Y   | T   |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | N   | A   | V   | Y   | D   | Y   | T   |
| Y                               | G   | S   | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | N   | L   | I   | Y   | D   | Y   | T   |
| Z                               | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | L   | D   | L   | I   | Y   | D   | Y   | T   |
| AA                              | A   | A   | N   | L   | T   | N   | A   | L   | T   | Y   | V   | C   | M   | L   | L   | Y   | D   | Y   | T   |
| BB                              | F   | L   | C   | V   | T   | Y   | S   | S   | S   | M   | L   | L   | N   | L   | L   | Y   | D   | Y   | T   |
| CC                              | F   | W   | A   | M   | T   | Y   | N   | T   | A   | Y   | L   | S   | G   | L   | M   | Y   | D   | Y   | T   |
| DD                              | Y   | M   | C   | V   | T   | F   | V   | S   | G   | M   | I   | L   | N   | F   | V   | Y   | D   | Y   | T   |
| EE                              | V   | S   | G   | Q   | T   | Y   | S   | V   | G   | L   | C   | W   | N   | L   | F   | Y   | D   | Y   | T   |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| HH                              | C   | A   | G   | T   | T   | M   | S   | T   | A   | L   | I   | G   | N   | T   | S   | Y   | D   | Y   | T   |
| II                              | I   | W   | V   | I   | S   | Y   | S   | T   | G   | M   | L   | I   | D   | L   | I   | Y   | D   | Y   | T   |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | N   | L   | I   | Y   | D   | Y   | T   |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| MM                              | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | Y   | D   | Y   | T   |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |



110. An isolated synthase having a region with 40% or greater sequence identity to residues 307 to 578 of SEQ ID NO: 50, wherein one or more amino acid residues of said synthase that align with amino acids at positions 312, 315, 336, 339, 340, 419, 444, 445, 446, 447, 450, 484, 488, 562, 565, 566, 570, 572 and 573 of SEQ ID NO: 50 are residues other than the following ordered arrangements of residues:

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 | 312 | 315 | 336 | 339 | 340 | 419 | 444 | 445 | 446 | 447 | 450 | 484 | 488 | 562 | 565 | 566 | 570 | 572 | 573 |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G   | W   | I   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | G   | N   | A   | V   | Y   | D   | Y   | T   |
| F                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | F   | D   | V   | L   | Y   | D   | F   | T   |
| G                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |
| H                               | L   | W   | I   | T   | T   | Y   | S   | V   | G   | N   | L   | G   | N   | C   | S   | Y   | D   | Y   | T   |
| I                               | P   | W   | I   | V   | D   | Y   | S   | T   | A   | G   | L   | S   | N   | I   | T   | Y   | D   | Y   | T   |
| J                               | A   | W   | V   | C   | G   | F   | E   | S   | T   | A   | M   | L   | D   | A   | M   | Y   | D   | H   | Q   |
| K                               | N   | F   | N   | L   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | V   | L   | Y   | D   | F   | T   |
| L                               | C   | W   | V   | L   | T   | Y   | S   | S   | S   | Y   | L   | G   | G   | A   | L   | Y   | D   | F   | T   |
| M                               | S   | W   | V   | L   | T   | Y   | S   | S   | L   | A   | L   | G   | N   | L   | S   | Y   | D   | F   | T   |
| N                               | N   | F   | F   | L   | V   | N   | A   | T   | L   | P   | L   | G   | N   | A   | Y   | D   | H   | G   | T   |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | G   | I   | L   | L   | D   | A   | M   | Y   | D   | F   | G   |
| P                               | C   | W   | N   | V   | T   | Y   | I   | G   | G   | L   | L   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| Q                               | C   | Y   | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | D   | G   |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | H   | G   |
| T                               | S   | W   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | G   |
| U                               | N   | W   | N   | L   | T   | Y   | S   | I   | S   | S   | I   | F   | N   | S   | M   | Y   | D   | H   | G   |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | H   | G   |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | M   | F   | Y   | D   | L   | T   |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | G   | F   | G   | Y   | D   | L   | T   |
| Y                               | G   | S   | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | N   | A   | V   | Y   | D   | H   | G   |
| Z                               | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | L   | Y   |
| AA                              | A   | A   | N   | L   | T   | N   | A   | L   | T   | S   | T   | C   | M   | L   | L   | Y   | D   | L   | Y   |
| BB                              | F   | L   | C   | V   | T   | Y   | S   | S   | A   | Y   | V   | L   | G   | L   | L   | Y   | D   | L   | Y   |
| CC                              | F   | W   | A   | M   | T   | Y   | S   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | L   | Y   |
| DD                              | Y   | M   | C   | V   | T   | F   | V   | S   | S   | G   | I   | L   | G   | F   | V   | Y   | D   | L   | Y   |
| EE                              | V   | S   | G   | Q   | V   | Y   | S   | V   | G   | L   | C   | W   | N   | V   | F   | Y   | D   | L   | Y   |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | L   | Y   |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | L   | Y   |
| HH                              | C   | A   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | L   | Y   |
| II                              | I   | W   | V   | I   | S   | Y   | T   | S   | G   | L   | V   | I   | N   | T   | S   | Y   | D   | L   | Y   |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | L   | Y   |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | L   | Y   |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | L   | Y   |
| MM                              | C   | W   | N   | I   | S   | Y   | T   | T   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | L   | Y   |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | L   | Y   |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | L   | Y   |

[illegible]

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 | 269 | 272 | 283 | 296 | 297 | 375 | 401 | 402 | 403 | 404 | 407 | 441 | 445 | 517 | 520 | 521 | 525 | 527 | 528 |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| E                               | C   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | G   | D   | A   | V   | Y   | D   | Y   | T   |
| F                               | G   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| G                               | C   | W   | L   | T   | S   | Y   | S   | V   | G   | N   | L   | F   | D   | V   | L   | Y   | D   | Y   | T   |
| H                               | L   | W   | I   | V   | D   | Y   | S   | T   | A   | N   | L   | S   | D   | A   | L   | Y   | D   | Y   | T   |
| I                               | P   | W   | I   | V   | D   | Y   | S   | T   | A   | N   | L   | S   | D   | A   | L   | Y   | D   | Y   | T   |
| J                               | A   | W   | F   | L   | G   | A   | E   | I   | T   | A   | T   | G   | N   | I   | S   | Y   | D   | Y   | T   |
| K                               | N   | C   | F   | L   | G   | A   | E   | I   | T   | A   | T   | G   | N   | I   | S   | Y   | D   | Y   | T   |
| L                               | C   | W   | N   | I   | T   | Y   | S   | S   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| M                               | S   | W   | V   | L   | T   | Y   | S   | S   | S   | Y   | L   | G   | D   | V   | L   | Y   | D   | Y   | T   |
| N                               | N   | F   | F   | L   | V   | N   | A   | T   | L   | A   | L   | G   | N   | L   | S   | Y   | D   | Y   | T   |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| P                               | C   | W   | N   | V   | T   | Y   | I   | G   | G   | I   | L   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| Q                               | C   | Y   | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | Y   | T   |
| T                               | S   | W   | I   | I   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |
| U                               | N   | W   | N   | L   | T   | Y   | S   | I   | S   | S   | I   | F   | N   | S   | M   | Y   | D   | Y   | T   |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | Y   | T   |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | M   | F   | Y   | D   | Y   | T   |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | G   | F   | G   | Y   | D   | Y   | T   |
| Y                               | G   | S   | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | N   | A   | V   | Y   | D   | Y   | T   |
| Z                               | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |
| AA                              | A   | A   | N   | L   | T   | N   | A   | L   | T   | Y   | T   | C   | M   | L   | L   | Y   | D   | Y   | T   |
| BB                              | F   | L   | C   | V   | T   | Y   | S   | S   | A   | Y   | V   | L   | G   | L   | L   | Y   | D   | Y   | T   |
| CC                              | F   | W   | A   | M   | T   | Y   | S   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | Y   | T   |
| DD                              | Y   | M   | C   | V   | T   | F   | V   | S   | S   | G   | I   | L   | G   | F   | V   | Y   | D   | Y   | T   |
| EE                              | V   | S   | G   | Q   | V   | Y   | S   | V   | G   | L   | C   | W   | N   | V   | F   | Y   | D   | Y   | T   |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | Y   | T   |
| HH                              | C   | A   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | Y   | T   |
| II                              | I   | W   | V   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | T   | S   | Y   | D   | Y   | T   |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | V   | I   | Y   | D   | Y   | T   |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| MM                              | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | Y   | T   |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | Y   | T   |

112. An isolated synthase having a region with 40% or greater sequence identity to residues 585 to 853 of SEQ ID NO: 56, wherein one or more amino acid residues of said synthase that align with amino acids at positions 590, 593, 614, 617, 618, 696, 721, 722, 723, 724, 727, 761, 765, 837, 840, 841, 845, 847 and 848 of SEQ ID NO: 56 are residues other than the following ordered arrangements of residues:

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 590                             | 593 | 614 | 617 | 618 | 696 | 721 | 722 | 723 | 724 | 727 | 761 | 765 | 837 | 840 | 841 | 845 | 847 | 848 |  |  |
| A                               | C   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |  |  |
| B                               | C   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |  |  |
| C                               | G   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |  |  |
| D                               | G   | I   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |  |  |
| E                               | C   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |  |  |
| F                               | G   | L   | T   | S   | Y   | S   | A   | V   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |  |  |
| G                               | C   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | L   | Y   | D   | Y   | T   |  |  |
| H                               | L   | I   | T   | T   | Y   | S   | V   | G   | N   | L   | F   | D   | V   | L   | Y   | D   | Y   | T   |  |  |
| I                               | P   | I   | V   | D   | Y   | S   | T   | A   | G   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |  |  |
| J                               | A   | V   | C   | G   | F   | T   | S   | C   | I   | M   | G   | N   | C   | S   | Y   | D   | Y   | T   |  |  |
| K                               | N   | F   | L   | G   | A   | E   | I   | T   | A   | T   | G   | N   | I   | T   | Y   | E   | F   | T   |  |  |
| L                               | C   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | Y   | T   |  |  |
| M                               | S   | V   | L   | T   | Y   | S   | S   | S   | Y   | L   | G   | G   | V   | L   | Y   | D   | H   | Q   |  |  |
| N                               | W   | F   | L   | V   | N   | A   | T   | L   | A   | L   | G   | N   | L   | S   | Y   | D   | F   | T   |  |  |
| O                               | C   | N   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | M   | Y   | D   | F   | T   |  |  |
| P                               | C   | N   | V   | T   | Y   | I   | G   | G   | I   | L   | L   | D   | A   | I   | Y   | D   | H   | T   |  |  |
| Q                               | Y   | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | G   |  |  |
| R                               | C   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | D   | T   |  |  |
| S                               | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | H   | G   |  |  |
| T                               | S   | I   | A   | T   | Y   | S   | S   | A   | S   | I   | L   | N   | A   | I   | Y   | D   | H   | G   |  |  |
| U                               | N   | N   | L   | T   | Y   | S   | I   | S   | Q   | L   | F   | N   | S   | M   | Y   | D   | F   | G   |  |  |
| V                               | F   | A   | Q   | T   | Y   | S   | I   | G   | L   | V   | S   | D   | T   | I   | F   | D   | H   | T   |  |  |
| W                               | L   | A   | T   | V   | Y   | S   | I   | A   | L   | S   | G   | N   | M   | F   | Y   | D   | L   | S   |  |  |
| X                               | S   | S   | T   | V   | Y   | S   | C   | G   | H   | S   | L   | N   | A   | G   | Y   | D   | H   | G   |  |  |
| Y                               | G   | F   | I   | T   | Y   | S   | S   | S   | V   | I   | L   | N   | L   | V   | Y   | D   | L   | S   |  |  |
| Z                               | W   | A   | C   | T   | N   | A   | S   | G   | M   | L   | G   | D   | A   | I   | Y   | D   | L   | G   |  |  |
| AA                              | A   | N   | L   | T   | N   | A   | L   | T   | S   | T   | C   | M   | L   | L   | Y   | D   | L   | S   |  |  |
| BB                              | F   | C   | V   | T   | Y   | S   | S   | A   | Y   | V   | L   | G   | L   | L   | Y   | D   | L   | S   |  |  |
| CC                              | F   | A   | M   | T   | Y   | S   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | L   | S   |  |  |
| DD                              | Y   | C   | V   | T   | F   | V   | S   | S   | G   | I   | L   | G   | F   | V   | Y   | D   | L   | S   |  |  |
| EE                              | V   | C   | Q   | V   | Y   | S   | V   | G   | L   | C   | W   | N   | L   | F   | Y   | D   | L   | S   |  |  |
| FF                              | C   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | L   | S   |  |  |
| GG                              | C   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | L   | S   |  |  |
| HH                              | C   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | L   | S   |  |  |
| II                              | I   | V   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | V   | T   | Y   | D   | L   | S   |  |  |
| JJ                              | Y   | A   | C   | T   | Y   | S   | S   | G   | M   | L   | G   | D   | L   | S   | Y   | D   | L   | S   |  |  |
| KK                              | C   | I   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | V   | T   | Y   | D   | L   | S   |  |  |
| LL                              | C   | I   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | V   | T   | Y   | D   | L   | S   |  |  |
| MM                              | C   | I   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | V   | T   | Y   | D   | L   | S   |  |  |
| NN                              | C   | I   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | V   | T   | Y   | D   | L   | S   |  |  |
| OO                              | F   | A   | Q   | T   | Y   | S   | I   | G   | Q   | M   | L   | D   | A   | M   | Y   | D   | L   | S   |  |  |
| PP                              | F   | A   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | L   | S   |  |  |

113. An isolated synthase having a region with 40% or greater sequence identity to residues 307 to 574 of SEQ ID NO: 54, wherein one or more amino acid residues of said synthase that align with amino acids at positions 312, 315, 336, 339, 340, 418, 443, 444, 445, 446, 449, 483, 487, 560, 563, 564, 566, 568 and 569 of SEQ ID NO: 54 are residues other than the following ordered arrangements of residues:

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 | 312 | 315 | 336 | 339 | 340 | 418 | 443 | 444 | 445 | 446 | 449 | 483 | 487 | 560 | 563 | 564 | 566 | 568 | 569 |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G   | W   | L   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | V   | Y   | D   | Y   | T   |
| F                               | G   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | G   | D   | A   | L   | Y   | D   | Y   | S   |
| G                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | F   | D   | V   | L   | Y   | D   | F   | T   |
| H                               | L   | W   | I   | V   | D   | Y   | S   | V   | G   | N   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |
| I                               | P   | W   | I   | C   | G   | F   | T   | A   | C   | I   | M   | G   | N   | C   | S   | Y   | D   | Y   | T   |
| J                               | A   | W   | V   | L   | G   | A   | E   | I   | T   | A   | T   | G   | N   | I   | T   | Y   | E   | F   | S   |
| K                               | N   | F   | N   | I   | T   | Y   | S   | S   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | F   | Q   |
| L                               | C   | W   | V   | L   | T   | Y   | S   | I   | S   | Y   | L   | G   | G   | V   | L   | Y   | D   | H   | T   |
| M                               | S   | W   | F   | L   | V   | N   | A   | T   | L   | A   | L   | G   | N   | L   | S   | Y   | E   | F   | T   |
| N                               | N   | F   | F   | L   | T   | Y   | S   | S   | A   | P   | L   | L   | D   | A   | M   | Y   | D   | F   | T   |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | G   | I   | L   | L   | D   | A   | I   | Y   | D   | H   | G   |
| P                               | C   | W   | N   | V   | T   | Y   | A   | G   | G   | L   | L   | L   | D   | A   | T   | Y   | D   | F   | G   |
| Q                               | C   | Y   | L   | L   | T   | F   | I   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | Y   | G   |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | D   | I   |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | H   | G   |
| T                               | S   | W   | I   | A   | T   | Y   | S   | S   | A   | S   | I   | L   | N   | A   | I   | Y   | D   | F   | G   |
| U                               | N   | W   | N   | L   | T   | Y   | S   | I   | S   | Q   | L   | S   | D   | T   | I   | F   | D   | H   | G   |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | G   | L   | V   | G   | N   | M   | I   | Y   | D   | L   | T   |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | S   | L   | G   | F   | V   | Y   | D   | Y   | S   |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | N   | A   | G   | Y   | D   | H   | G   |
| Y                               | G   | S   | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | D   | L   | I   | Y   | D   | L   | Y   |
| Z                               | Y   | W   | A   | C   | T   | Y   | S   | S   | G   | M   | T   | C   | M   | L   | L   | Y   | D   | L   | N   |
| AA                              | A   | A   | N   | L   | T   | N   | A   | L   | T   | S   | T   | L   | G   | L   | L   | Y   | D   | Y   | S   |
| BB                              | F   | L   | C   | V   | T   | Y   | S   | A   | Y   | V   | L   | C   | D   | L   | L   | Y   | D   | F   | S   |
| CC                              | F   | W   | A   | M   | T   | Y   | N   | G   | M   | L   | L   | G   | M   | L   | L   | Y   | D   | F   | S   |
| DD                              | Y   | M   | C   | V   | T   | Y   | V   | S   | G   | L   | C   | L   | G   | I   | M   | Y   | D   | Y   | T   |
| EE                              | V   | S   | G   | Q   | V   | F   | S   | V   | G   | L   | V   | L   | G   | V   | F   | Y   | D   | Y   | G   |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | F   | T   |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | L   | I   | I   | G   | N   | L   | F   | Y   | D   | F   | T   |
| HH                              | C   | A   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | Y   | T   |
| II                              | I   | W   | V   | I   | S   | Y   | T   | G   | L   | L   | V   | I   | N   | T   | S   | Y   | D   | L   | Y   |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | T   | M   | L   | L   | G   | D   | L   | I   | Y   | D   | Y   | T   |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | T   | Y   | L   | C   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | T   | Y   | L   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| MM                              | C   | W   | N   | I   | T   | Y   | S   | T   | G   | M   | L   | C   | D   | L   | M   | Y   | D   | H   | G   |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | A   | M   | Y   | D   | F   | G   |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | A   | S   | L   | I   | L   | D   | T   | I   | Y   | D   | F   | G   |



114. An isolated synthase having a region with 40% or greater sequence identity to residues 309 to 577 of SEQ ID NO: 24, wherein one or more amino acid residues of said synthase that align with amino acids at positions 314, 317, 338, 341, 342, 420, 446, 447, 448, 449, 452, 485, 489, 560, 563, 564, 569, 571 and 572 of SEQ ID NO: 24 are residues other than the following ordered arrangements of residues:

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 | 314 | 317 | 338 | 341 | 342 | 420 | 446 | 447 | 448 | 449 | 452 | 485 | 489 | 560 | 563 | 564 | 569 | 571 | 572 |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | L   | Y   | D   | Y   | T   |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G   | W   | I   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| F                               | G   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | G   | D   | A   | V   | Y   | D   | Y   | T   |
| G                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| H                               | L   | W   | I   | T   | T   | Y   | S   | V   | G   | Y   | L   | F   | D   | V   | L   | Y   | D   | F   | T   |
| I                               | P   | W   | I   | V   | D   | Y   | S   | T   | A   | G   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |
| J                               | A   | W   | V   | C   | G   | F   | T   | S   | C   | I   | M   | G   | N   | C   | S   | Y   | D   | Y   | T   |
| K                               | N   | F   | F   | L   | G   | A   | E   | I   | T   | A   | T   | G   | N   | I   | T   | Y   | E   | F   | T   |
| L                               | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | T   |
| M                               | S   | W   | V   | L   | T   | Y   | S   | S   | Y   | Y   | L   | G   | G   | V   | L   | Y   | D   | F   | T   |
| N                               | N   | F   | F   | L   | V   | N   | A   | T   | L   | A   | L   | G   | N   | L   | S   | Y   | D   | F   | T   |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | M   | Y   | D   | H   | T   |
| P                               | C   | W   | N   | V   | T   | Y   | I   | G   | G   | I   | L   | L   | D   | A   | I   | Y   | D   | F   | T   |
| Q                               | C   | Y   | L   | L   | T   | F   | A   | V   | T   | M   | T   | G   | N   | I   | T   | Y   | D   | F   | T   |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | D   | T   |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | H   | T   |
| T                               | S   | W   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | T   |
| U                               | N   | W   | N   | L   | T   | Y   | S   | I   | S   | S   | I   | F   | N   | A   | M   | Y   | D   | H   | T   |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | F   | T   |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | M   | F   | Y   | D   | L   | T   |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | G   | F   | G   | Y   | D   | H   | T   |
| Y                               | G   | S   | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | N   | A   | V   | Y   | D   | L   | T   |
| Z                               | Y   | W   | A   | C   | T   | Y   | S   | S   | S   | M   | L   | G   | D   | L   | I   | Y   | D   | L   | T   |
| AA                              | A   | A   | N   | L   | T   | N   | A   | L   | T   | S   | T   | C   | M   | L   | L   | Y   | D   | L   | T   |
| BB                              | F   | L   | C   | V   | T   | Y   | S   | S   | A   | Y   | V   | L   | G   | L   | L   | Y   | D   | F   | T   |
| CC                              | F   | W   | A   | M   | T   | Y   | N   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | F   | T   |
| DD                              | Y   | M   | C   | V   | T   | F   | V   | S   | G   | G   | I   | L   | G   | F   | V   | Y   | D   | F   | T   |
| EE                              | V   | S   | G   | Q   | V   | Y   | S   | V   | S   | L   | C   | W   | N   | V   | V   | Y   | D   | Y   | T   |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | F   | T   |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | F   | T   |
| HH                              | C   | A   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | Y   | T   |
| II                              | I   | W   | V   | I   | S   | Y   | T   | T   | G   | L   | V   | I   | N   | T   | S   | Y   | D   | Y   | T   |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | T   | M   | Y   | L   | G   | D   | L   | I   | Y   | D   | L   | T   |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | T   | Y   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | T   | Y   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| MM                              | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | T   |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | F   | T   |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | T   |

115. An isolated synthase having a region with 40% or greater sequence identity to residues 315 to 584 of SEQ ID NO: 26, wherein one or more amino acid residues of said synthase that align with amino acids at positions 320, 323, 344, 347, 348, 426, 451, 452, 453, 454, 457, 492, 496, 568, 571, 572, 576, 578 and 579 of SEQ ID NO: 26 are residues other than the following ordered arrangements of residues:

| Residue | 320 | 323 | 344 | 347 | 348 | 426 | 451 | 452 | 453 | 454 | 457 | 492 | 496 | 568 | 571 | 572 | 576 | 578 | 579 |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| A       | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B       | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| C       | G   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| D       | G   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| E       | G   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| F       | G   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| G       | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| H       | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| I       | L   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| J       | P   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| K       | A   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| L       | N   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| M       | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| N       | S   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| O       | N   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| P       | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| Q       | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| R       | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| S       | S   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| T       | S   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| U       | N   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| V       | F   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| W       | I   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| X       | Y   | S   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| Y       | G   | L   | A   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| Z       | Y   | S   | A   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| AA      | A   | W   | A   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| BB      | F   | L   | C   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| CC      | F   | W   | A   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| DD      | V   | M   | C   | I   | S   | Y   | T   | T   | T   |     |     |     |     |     |     |     |     |     |     |

116. An isolated synthase having a region with 40% or greater sequence identity to residues 265 to 536 of SEQ ID NO: 28, wherein one or more amino acid residues of said synthase that align with amino acids at positions 270, 273, 294, 297, 298, 376, 401, 402, 403, 404, 407, 440, 444, 518, 521, 522, 528, 530 and 531 of SEQ ID NO: 28 are residues other than the following ordered arrangements of residues:

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117. An isolated synthase having a region with 40% or greater sequence identity to residues 342 to 612 of SEQ ID NO: 30, wherein one or more amino acid residues of said synthase that align with amino acids at positions 347, 350, 371, 374, 375, 453, 478, 479, 480, 481, 483, 518, 522, 596, 599, 600, 604, 606 and 607 of SEQ ID NO: 30 are residues other than the following ordered arrangements of residues:

| Ordered Arrangement of Residues |   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 |   | 347 | 350 | 371 | 374 | 375 | 453 | 478 | 479 | 480 | 481 | 483 | 518 | 522 | 596 | 599 | 600 | 604 | 606 | 607 |
| A                               | C | C   | W   | I   | I   | S   | Y   | T   | T   | Y   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C | W   | W   | I   | I   | S   | Y   | T   | T   | Y   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G | W   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G | W   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| E                               | C | W   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | G   | D   | A   | V   | Y   | D   | Y   | T   |
| F                               | C | W   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | A   | N   | A   | L   | Y   | D   | Y   | T   |
| G                               | C | W   | W   | L   | T   | S   | Y   | S   | V   | G   | N   | L   | F   | D   | V   | L   | Y   | D   | F   | T   |
| H                               | L | W   | W   | I   | T   | T   | Y   | S   | T   | A   | G   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |
| I                               | P | W   | W   | V   | C   | G   | F   | T   | S   | I   | M   | G   | G   | N   | I   | S   | Y   | D   | Y   | T   |
| J                               | A | W   | W   | F   | L   | G   | A   | E   | I   | A   | T   | M   | L   | D   | A   | T   | Y   | E   | F   | T   |
| K                               | N | C   | W   | N   | I   | T   | Y   | S   | I   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | T   |
| L                               | C | W   | W   | V   | L   | T   | Y   | S   | S   | Y   | Y   | L   | G   | G   | V   | L   | Y   | D   | F   | T   |
| M                               | S | W   | W   | L   | L   | V   | N   | A   | T   | A   | L   | L   | G   | N   | L   | S   | Y   | D   | F   | T   |
| N                               | N | F   | F   | L   | I   | T   | Y   | I   | S   | P   | P   | L   | L   | D   | A   | M   | Y   | D   | H   | T   |
| O                               | C | W   | W   | N   | V   | T   | Y   | I   | G   | I   | L   | L   | L   | D   | A   | I   | Y   | D   | F   | T   |
| P                               | C | W   | W   | N   | L   | T   | F   | A   | V   | M   | T   | T   | G   | N   | I   | T   | Y   | D   | Y   | T   |
| Q                               | C | Y   | L   | L   | L   | T   | Y   | S   | I   | A   | I   | L   | L   | D   | A   | I   | Y   | D   | D   | T   |
| R                               | C | W   | W   | I   | I   | T   | Y   | S   | S   | V   | V   | I   | L   | N   | V   | I   | Y   | D   | H   | T   |
| S                               | S | W   | W   | F   | I   | V   | F   | S   | S   | S   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | T   |
| T                               | S | W   | W   | I   | A   | T   | Y   | S   | A   | S   | S   | I   | L   | D   | A   | I   | Y   | D   | H   | T   |
| U                               | N | W   | W   | N   | L   | T   | Y   | S   | I   | S   | Q   | L   | F   | N   | S   | M   | Y   | D   | F   | T   |
| V                               | F | L   | L   | A   | Q   | T   | Y   | S   | I   | G   | L   | V   | S   | D   | T   | I   | F   | D   | L   | T   |
| W                               | I | S   | L   | S   | T   | V   | Y   | S   | I   | A   | L   | S   | G   | N   | M   | F   | Y   | D   | Y   | T   |
| X                               | Y | L   | S   | C   | I   | T   | F   | S   | C   | G   | H   | S   | L   | G   | F   | G   | Y   | D   | H   | T   |
| Y                               | G | S   | W   | F   | I   | T   | Y   | S   | S   | S   | V   | I   | L   | N   | A   | V   | Y   | D   | L   | T   |
| Z                               | Y | Y   | W   | A   | C   | T   | Y   | S   | S   | M   | M   | L   | G   | D   | L   | I   | Y   | D   | L   | T   |
| AA                              | A | A   | A   | N   | L   | T   | N   | A   | L   | S   | T   | T   | C   | M   | L   | L   | Y   | D   | Y   | T   |
| BB                              | F | L   | L   | C   | V   | T   | Y   | S   | A   | Y   | Y   | V   | L   | G   | L   | L   | Y   | D   | F   | T   |
| CC                              | F | W   | M   | A   | M   | T   | Y   | S   | G   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | F   | T   |
| DD                              | Y | M   | C   | C   | V   | T   | Y   | S   | S   | L   | G   | C   | W   | N   | V   | V   | Y   | D   | Y   | T   |
| EE                              | V | S   | S   | G   | Q   | T   | Y   | S   | V   | G   | L   | V   | L   | G   | F   | F   | Y   | D   | Y   | T   |
| FF                              | C | S   | S   | G   | T   | T   | M   | F   | A   | L   | G   | I   | G   | N   | L   | F   | Y   | D   | F   | T   |
| GG                              | C | S   | S   | G   | T   | T   | M   | S   | A   | A   | L   | I   | G   | N   | L   | F   | Y   | D   | F   | T   |
| HH                              | C | A   | W   | V   | I   | S   | Y   | T   | G   | L   | L   | V   | I   | N   | T   | S   | Y   | D   | Y   | T   |
| II                              | I | W   | W   | A   | C   | T   | Y   | S   | G   | M   | M   | L   | G   | D   | L   | I   | Y   | D   | L   | T   |
| JJ                              | Y | W   | W   | A   | I   | S   | Y   | S   | G   | L   | Y   | L   | C   | D   | V   | I   | Y   | D   | Y   | T   |
| KK                              | C | W   | W   | I   | I   | S   | Y   | T   | T   | Y   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| LL                              | C | W   | W   | I   | I   | S   | Y   | T   | T   | Y   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| MM                              | C | W   | W   | N   | I   | T   | Y   | S   | I   | G   | Q   | M   | L   | D   | A   | M   | Y   | D   | H   | T   |
| NN                              | F | A   | A   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | F   | T   |
| OO                              | F | A   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | T   |



118. An isolated synthase having a region with about 40% or greater sequence identity to residues 307 to 541 of SEQ ID NO: 32, wherein one or more amino acid residues of said synthase that align with amino acids at positions 278, 281, 302, 305, 306, 384, 409, 410, 411, 412, 415, 448, 452, 524, 527, 528, 533, 535 and 536 of SEQ ID NO: 32 are residues other than the following ordered arrangements of residues:

| Ordered Arrangement of Residues |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                 | 278 | 281 | 302 | 305 | 306 | 384 | 409 | 410 | 411 | 412 | 415 | 448 | 452 | 524 | 527 | 528 | 533 | 535 | 536 |
| A                               | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| B                               | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| C                               | G   | W   | I   | A   | S   | Y   | T   | C   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| D                               | G   | W   | L   | A   | S   | Y   | T   | S   | G   | Y   | L   | C   | D   | M   | L   | Y   | D   | Y   | T   |
| E                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | I   | A   | N   | A   | V   | Y   | D   | Y   | S   |
| F                               | G   | W   | L   | L   | S   | Y   | S   | T   | V   | H   | L   | A   | N   | A   | L   | Y   | D   | Y   | S   |
| G                               | C   | W   | L   | T   | S   | Y   | S   | A   | G   | Y   | L   | F   | D   | V   | L   | Y   | D   | F   | T   |
| H                               | L   | W   | I   | T   | T   | Y   | S   | V   | G   | N   | L   | S   | D   | A   | C   | Y   | D   | Y   | T   |
| I                               | P   | W   | I   | V   | D   | Y   | S   | T   | A   | G   | L   | S   | D   | V   | L   | Y   | D   | Y   | T   |
| J                               | A   | W   | V   | C   | G   | F   | T   | S   | C   | I   | M   | G   | N   | I   | T   | Y   | E   | F   | T   |
| K                               | N   | F   | L   | L   | G   | A   | E   | I   | T   | A   | M   | L   | D   | A   | M   | Y   | D   | H   | Q   |
| L                               | C   | W   | N   | I   | T   | Y   | S   | S   | S   | G   | M   | L   | G   | V   | L   | Y   | D   | F   | T   |
| M                               | S   | W   | V   | L   | L   | Y   | S   | S   | S   | Y   | L   | G   | N   | L   | S   | Y   | E   | F   | T   |
| N                               | N   | F   | L   | L   | V   | N   | A   | T   | L   | A   | L   | L   | G   | L   | M   | Y   | D   | H   | G   |
| O                               | C   | W   | N   | I   | T   | Y   | I   | S   | G   | P   | L   | L   | D   | A   | A   | Y   | D   | F   | G   |
| P                               | C   | W   | N   | V   | T   | Y   | I   | G   | G   | I   | L   | L   | D   | A   | I   | Y   | D   | F   | G   |
| Q                               | C   | Y   | L   | L   | T   | F   | A   | V   | T   | M   | T   | L   | N   | I   | T   | Y   | D   | Y   | I   |
| R                               | C   | W   | I   | I   | T   | Y   | S   | I   | S   | A   | I   | L   | D   | A   | I   | Y   | D   | D   | G   |
| S                               | S   | W   | F   | I   | V   | F   | S   | S   | S   | V   | I   | L   | N   | V   | I   | Y   | D   | H   | G   |
| T                               | S   | W   | I   | A   | T   | Y   | S   | S   | S   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | G   |
| U                               | N   | W   | L   | N   | L   | Y   | S   | I   | S   | S   | I   | F   | N   | S   | M   | Y   | D   | H   | G   |
| V                               | F   | L   | A   | Q   | T   | Y   | S   | I   | G   | Q   | L   | S   | D   | T   | I   | F   | D   | F   | G   |
| W                               | I   | S   | S   | T   | V   | Y   | S   | I   | A   | L   | V   | G   | N   | M   | F   | Y   | D   | L   | S   |
| X                               | Y   | L   | C   | I   | T   | Y   | S   | C   | G   | H   | S   | L   | N   | A   | V   | Y   | D   | H   | G   |
| Y                               | G   | S   | F   | I   | T   | F   | S   | S   | S   | V   | I   | L   | D   | L   | I   | Y   | D   | L   | Y   |
| Z                               | Y   | W   | A   | C   | T   | N   | A   | L   | T   | S   | L   | L   | G   | L   | I   | Y   | D   | L   | Y   |
| AA                              | A   | A   | N   | L   | T   | Y   | S   | S   | G   | M   | L   | L   | D   | L   | L   | Y   | D   | Y   | N   |
| BB                              | F   | L   | C   | V   | T   | Y   | S   | S   | A   | Y   | V   | L   | G   | L   | L   | Y   | D   | F   | S   |
| CC                              | F   | W   | A   | M   | T   | Y   | N   | T   | G   | M   | L   | S   | D   | I   | M   | Y   | D   | F   | S   |
| DD                              | Y   | M   | C   | V   | T   | F   | V   | S   | G   | I   | C   | W   | N   | V   | F   | Y   | D   | Y   | G   |
| EE                              | V   | S   | G   | Q   | T   | Y   | S   | V   | G   | L   | C   | N   | L   | L   | F   | Y   | D   | F   | T   |
| FF                              | C   | S   | G   | T   | T   | M   | F   | A   | L   | G   | V   | G   | N   | L   | F   | Y   | D   | F   | T   |
| GG                              | C   | S   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | Y   | T   |
| HH                              | C   | A   | G   | T   | T   | M   | S   | F   | A   | L   | I   | G   | N   | V   | F   | Y   | D   | Y   | T   |
| II                              | I   | W   | V   | I   | S   | Y   | T   | G   | L   | V   | L   | I   | N   | T   | S   | Y   | D   | Y   | T   |
| JJ                              | Y   | W   | A   | C   | T   | Y   | S   | G   | M   | L   | L   | G   | D   | L   | I   | Y   | D   | L   | Y   |
| KK                              | C   | W   | I   | I   | S   | Y   | T   | S   | T   | Y   | L   | C   | D   | V   | T   | Y   | D   | Y   | T   |
| LL                              | C   | W   | I   | I   | S   | Y   | T   | T   | T   | Y   | L   | C   | D   | I   | T   | Y   | D   | Y   | T   |
| MM                              | C   | W   | N   | I   | T   | Y   | S   | T   | S   | G   | M   | L   | D   | A   | M   | Y   | D   | H   | G   |
| NN                              | F   | A   | A   | Q   | T   | Y   | S   | I   | S   | Q   | L   | S   | D   | T   | I   | F   | D   | F   | G   |
| OO                              | F   | A   | I   | A   | T   | Y   | S   | V   | A   | S   | I   | L   | D   | A   | I   | Y   | D   | F   | G   |

119. A method for making a terpene synthase, comprising:  
a) identifying, in a preselected polypeptide having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, nine amino acid residues whose  $\alpha$ -carbons have interatomic distances in Angstroms between said  $\alpha$ -carbons that are  $\pm 2.3$  Angstroms of the following interatomic distances:

| $\alpha$ -Carbon | 1    | 2    | 3    | 4    | 5    | 6    | 7    | 8    | 9    |
|------------------|------|------|------|------|------|------|------|------|------|
| 1                | 0.0  | 8.4  | 13.7 | 12.7 | 11.9 | 10.2 | 13.1 | 9.4  | 12.8 |
| 2                | 8.4  | 0.0  | 11.3 | 8.7  | 10.2 | 7.2  | 14.8 | 15.1 | 17.4 |
| 3                | 13.7 | 11.3 | 0.0  | 3.8  | 5.4  | 9.3  | 6.6  | 13.9 | 13.7 |
| 4                | 12.7 | 8.7  | 3.8  | 0.0  | 3.8  | 6.0  | 9.2  | 15.4 | 16.1 |
| 5                | 11.9 | 10.2 | 5.4  | 3.8  | 0.0  | 5.0  | 7.8  | 14.6 | 15.5 |
| 6                | 10.2 | 7.2  | 9.3  | 6.0  | 5.0  | 0.0  | 12.0 | 16.1 | 18.0 |
| 7                | 13.1 | 14.8 | 6.6  | 9.2  | 7.8  | 12.0 | 0.0  | 10.2 | 9.5  |
| 8                | 9.4  | 15.1 | 13.9 | 15.4 | 14.6 | 16.1 | 10.2 | 0.0  | 3.8  |
| 9                | 12.8 | 17.4 | 13.7 | 16.1 | 15.5 | 18.0 | 9.5  | 3.8  | 0.0  |

the center point of each said  $\alpha$ -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center point of each said sphere having the following structural coordinates:

| $\alpha$ -Carbon Number | X Position | Y Position | Z Position |
|-------------------------|------------|------------|------------|
| 1                       | 120.203    | 38.695     | 43.506     |
| 2                       | 114.058    | 43.884     | 41.015     |
| 3                       | 106.807    | 36.336     | 45.151     |
| 4                       | 107.629    | 38.010     | 41.804     |
| 5                       | 109.375    | 34.842     | 40.617     |
| 6                       | 111.944    | 37.854     | 37.602     |
| 7                       | 110.233    | 31.098     | 47.361     |
| 8                       | 118.846    | 34.443     | 51.796     |
| 9                       | 116.461    | 32.848     | 54.290     |

; and

b) synthesizing a polypeptide that is modified from said preselected polypeptide, said modified polypeptide having one or more R-groups associated with said  $\alpha$ -carbons other than the R-groups associated with said  $\alpha$ -carbons in said preselected polypeptide, wherein said modified polypeptide has terpene synthase activity.

120. The method of claim 119, wherein said synthesizing step comprises the formation of a nucleic acid encoding said preselected polypeptide in which the coding sequence for one or more amino acids corresponding to said nine  $\alpha$ -carbons is replaced by a coding sequence that codes for an amino acid different from the amino acid present in said preselected polypeptide.

121. The method of claim 119, wherein said preselected polypeptide is a pinene synthase.

122. The method of claim 121, wherein said preselected polypeptide is SEQ ID NO: 20.

123. The method of claim 119, wherein said preselected polypeptide is a taxadiene synthase.

124. The method of claim 123, wherein said preselected polypeptide is SEQ ID NO: 44.

125. A method of using a terpene synthase, comprising:

a) identifying, in a preselected polypeptide having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, amino acid residues at nine positions that align with amino acid residues at positions 273, 294, 402, 403, 404, 407, 440, 519 and 520 of SEQ ID NO: 2; and

b) synthesizing a polypeptide that is modified from said preselected polypeptide, said modified polypeptide having amino acid residues at one or more of said nine positions other than the amino acid residues present in said preselected polypeptide.

126. The method of claim 125, wherein said identifying step comprises identifying sixteen amino acid residues in said preselected polypeptide that align with amino acid residues at positions 270, 273, 294, 297, 298, 402, 403, 404, 407, 440, 516, 519, 520, 525, 527 and 528 of SEQ ID NO: 2, and said synthesizing step comprises synthesizing a polypeptide that is modified from said preselected polypeptide, said modified polypeptide having amino acid residues at one or more of said sixteen positions other than the amino acid residues present in said preselected polypeptide.



134. The method of claim 133, wherein said isoprenoid substrate is a geranyl diphosphate.

135 The method of claim 133, wherein said isoprenoid substrate is a farnesyl diphosphate.

136. The method of claim 133, wherein said isoprenoid substrate is a geranyl genanyl diphosphate.

137. A method of making a terpene synthase, comprising:  
creating a population of nucleic acid molecules that encode polypeptides, said population having members that differ from one another at one or more of nine codons specifying amino acids in a region of a preselected terpene synthase polypeptide having 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2,  $\alpha$ -carbons of said nine amino acids having interatomic distances in Angstroms between said  $\alpha$ -carbons that are  $\pm 2.3$  Angstroms of the following interatomic distances:

| $\alpha$ -Carbon | 1    | 2    | 3    | 4    | 5    | 6    | 7    | 8    | 9    |
|------------------|------|------|------|------|------|------|------|------|------|
| 1                | 0.0  | 8.4  | 13.7 | 12.7 | 11.9 | 10.2 | 13.1 | 9.4  | 12.8 |
| 2                | 8.4  | 0.0  | 11.3 | 8.7  | 10.2 | 7.2  | 14.8 | 15.1 | 17.4 |
| 3                | 13.7 | 11.3 | 0.0  | 3.8  | 5.4  | 9.3  | 6.6  | 13.9 | 13.7 |
| 4                | 12.7 | 8.7  | 3.8  | 0.0  | 3.8  | 6.0  | 9.2  | 15.4 | 16.1 |
| 5                | 11.9 | 10.2 | 5.4  | 3.8  | 0.0  | 5.0  | 7.8  | 14.6 | 15.5 |
| 6                | 10.2 | 7.2  | 9.3  | 6.0  | 5.0  | 0.0  | 12.0 | 16.1 | 18.0 |
| 7                | 13.1 | 14.8 | 6.6  | 9.2  | 7.8  | 12.0 | 0.0  | 10.2 | 9.5  |
| 8                | 9.4  | 15.1 | 13.9 | 15.4 | 14.6 | 16.1 | 10.2 | 0.0  | 3.8  |
| 9                | 12.8 | 17.4 | 13.7 | 16.1 | 15.5 | 18.0 | 9.5  | 3.8  | 0.0  |

the center point of each said  $\alpha$ -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center point of each said sphere having the following structural coordinates:

| $\alpha$ -Carbon Number | X Position | Y Position | Z Position |
|-------------------------|------------|------------|------------|
| 1                       | 120.203    | 38.695     | 43.506     |
| 2                       | 114.058    | 43.884     | 41.015     |
| 3                       | 106.807    | 36.336     | 45.151     |
| 4                       | 107.629    | 38.010     | 41.804     |
| 5                       | 109.375    | 34.842     | 40.617     |
| 6                       | 111.944    | 37.854     | 37.602     |
| 7                       | 110.233    | 31.098     | 47.361     |
| 8                       | 118.846    | 34.443     | 51.796     |
| 9                       | 116.461    | 32.848     | 54.290     |

; and

b) expressing at least a portion of said nucleic acid population so that a population of polypeptides is made, wherein at least one member of said population of polypeptides is a mutant terpene synthase.

138. The method of claim 137, wherein said expressing step comprises *in vitro* transcription and *in vitro* translation of said nucleic acid populations.

139. The method of claim 137, wherein said expressing step comprises:

- i) cloning said members of said nucleic acid population into an expression vector;
- ii) introducing, into host cells, said cloned nucleic acid population members in said expression vector; and
- iii) expressing said cloned nucleic acid population members in said host cells so that said population of polypeptides is made.

140. The method of claim 139, wherein said host cells are prokaryotic cells.

141. The method of claim 137, wherein said preselected terpene synthase polypeptide is a monoterpene synthase.

142. The method of claim 137, wherein said preselected terpene synthase polypeptide is a sesquiterpene synthase.

143. The method of claim 137, wherein said preselected terpene synthase polypeptide is a diterpene synthase.
144. An isolated nucleic acid encoding the synthase of claim 1.
145. An isolated nucleic acid encoding the synthase of claim 2.
146. An isolated nucleic acid encoding the synthase of claim 3.
147. An isolated nucleic acid encoding the synthase of claim 7.
148. An isolated nucleic acid encoding a synthase selected from the group consisting of the synthase of claims 11 through 73.
149. An isolated nucleic acid encoding the synthase of claim 80.
150. An isolated nucleic acid encoding the synthase of claim 88.
151. An isolated nucleic acid encoding the synthase of claim 95.
152. An isolated nucleic acid encoding a synthase selected from the group consisting of the synthase of claims 102 through 118.
153. A host cell containing a nucleic acid encoding the synthase of claim 1.
154. The host cell of claim 153, wherein said cell is a prokaryotic cell.
155. The host cell of claim 153, wherein said cell is a eukaryotic cell.
156. The host cell of claim 155, wherein said cell is an insect cell.
157. The host cell of claim 155, wherein said cell is a plant cell.
158. The host cell of claim 157, wherein said host cell is an Angiosperm cell.



159. The host cell of claim 157, wherein said host cell is an Gymnosperm cell.

160. The host cell of claim 157, wherein said host cell is selected from the group consisting of: a cell from a Graminaceae plant, a cell from a Legumineae plant, a cell from a Solanaceae plant, a cell from a Brassicaeae plant and a cell from a Conifereae plant.

161. A transgenic plant containing a nucleic acid encoding the synthase of claim 1.

162. A transgenic animal cell culture containing a nucleic acid encoding the synthase of claim 1.